

STIC-Biotech/ChemLib**94073**

From: Schultz, James
Sent: Thursday, May 15, 2003 7:52 AM
To: STIC-Biotech/ChemLib
Subject: Seq Search 09/780,929

RECEIVED

MAY 15 2003

DIALOG/STIC/ChemLib
(STIC)

Hello,
Could you please run a length limited nucleotide sequence search on SEQ ID NOS: 97 (15 nt long) and 98 (18 nt long) in the above entitled case, where the maximum size of the returned hit is no longer than 20 nucleotides long?
Thanks,
Doug Schultz

STIC-Biotech/ChemLib**94073**

From: Schultz, James
Sent: Thursday, May 15, 2003 7:53 AM
To: STIC-Biotech/ChemLib
Subject: But wait there's more--Seq Search 09/780,929

RECEIVED

MAY 15 2003

DIALOG/STIC/ChemLib
(STIC)

The sequence search request below was just submitted--I forgot to include that I also need the interference databases searched. Thanks,
Doug Schultz

-----Original Message-----

From: Schultz, James
Sent: Thursday, May 15, 2003 7:52 AM
To: STIC-Biotech/ChemLib
Subject: Seq Search 09/780,929

Hello,
Could you please run a length limited nucleotide sequence search on SEQ ID NOS: 97 (15 nt long) and 98 (18 nt long) in the above entitled case, where the maximum size of the returned hit is no longer than 20 nucleotides long?
Thanks,
Doug Schultz

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 5/16
Date Completed: 5/25
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.4-p5-4578
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Om nucleic - nucleic search, using sw model

score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Run on: May 22, 2003, 16:53:27 ; Search time 871.364 Seconds
 (without alignments)
 500.987 Million cell updates/sec

Title: US-09-780-929-97
 Perfect score: 15
 Sequence: 1 agauacgugaagau 15

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched:

2054640 seqs, 14551402878 residues
 Total number of hits satisfying chosen parameters: 332216

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

Result No.	Score	Query Match	Length	DB ID	Description
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2	12	80.0	17	6 AX225565	AX225565 Sequence
3	12	80.0	17	6 AX225566	AX225566 Sequence
4	11	73.3	20	6 AX254729	AX254729 Sequence
5	11	73.3	20	6 AX255079	AX255079 Sequence
6	10.8	72.0	20	6 AX296064	AX296064 Sequence
7	10.8	72.0	20	6 AX304787	AX304787 Sequence
8	10.4	69.3	16	6 AX349237	AX349237 Sequence
9	10.4	69.3	17	6 AX349231	AX349231 Sequence
10	10.4	69.3	17	6 AX372471	AX372471 Sequence
11	10.4	69.3	17	6 AX372472	AX372472 Sequence
12	10.4	69.3	17	6 AX372653	AX372653 Sequence
13	10.4	69.3	17	6 AX372793	AX372793 Sequence
14	10.4	69.3	17	6 AX399883	AX399883 Sequence
15	10.4	69.3	17	6 AX325561	AX325561 Sequence
16	10.4	69.3	17	6 AX325562	AX325562 Sequence
17	10.2	68.0	15	6 AR033681	AR033681 Sequence
18	10.2	68.0	15	6 AR113033	AR113033 Sequence
19	10.2	68.0	15	6 AR15910	AR15910 Sequence
20	10.2	68.0	19	6 AR038557	AR038557 Sequence
21	10	66.7	16	6 A89154	A89154 Sequence
22	10	66.7	17	6 AX372473	AX372473 Sequence
23	10	66.7	18	6 AX110432	AX110432 Sequence
24	10	66.7	20	6 AX020035	AX020035 Sequence
25	10	66.7	20	6 AX295533	AX295533 Sequence
26	9.8	65.3	14	6 A13614	A13614 Oligonucleo
27	9.8	65.3	14	6 T0009	T0009 Sequence
28	9.8	65.3	15	6 E33049	E33049 Antisense o
29	9.8	65.3	17	6 AR040477	AR040477 Sequence
30	9.8	65.3	17	6 AX227367	AX227367 Sequence
31	9.8	65.3	17	6 AX227587	AX227587 Sequence
32	9.8	65.3	18	6 A02405	A02405 Oligonucleo
33	9.8	65.3	18	6 AR106822	AR106822 Sequence
34	9.8	65.3	18	6 AR131036	AR131036 Sequence
35	9.8	65.3	19	6 AX131037	AX131037 Sequence
36	9.8	65.3	19	6 AR206662	AR206662 Sequence
37	9.8	65.3	20	6 AX148986	AX148986 Sequence
38	9.8	65.3	20	6 AX462386	AX462386 Sequence
39	9.8	65.3	20	6 AR162930	AR162930 Sequence
40	9.6	64.0	17	6 AR167259	AR167259 Sequence
41	9.6	64.0	17	6 AR206920	AR206920 Sequence
42	9.6	64.0	17	6 I33759	I33759 Sequence
43	9.6	64.0	17	6 I36972	I36972 Sequence
44	9.6	64.0	17	6 AR132924	AR132924 Sequence

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a

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SOURCE	1. .15 /organism="synthetic construct" /db_xref="taxon:32630" /note="Nucleic Acid"
BASE COUNT	7 a 1 c 4 g 3 t
ORIGIN	
QY	1 AGAUACCGUGAAGAU 15 : : : : Db 1 AGATAACGTGAAT 15
Query Match	100.0%; Score 15; DB 6; Length 15;
Best Local Similarity	80.0%; Pred. No. 9.9e-02;
Matches	12; Conservative 3; Mismatches 0;
Indels	0; Gaps 0;
RESULT 2	
AX254565	
LOCUS	AX325565 17 bp DNA
DEFINITION	Sequence 17/03 from Patent WO0192512.
ACCESSION	AX325565
VERSION	AX325565.1 GI:1809632
KEYWORDS	Beta vulgaris
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
REFERENCE	Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
AUTHORS	Targeted chromosomal genomic alterations in plants using modified
TITLE	single stranded oligonucleotides
JOURNAL	Patent: WO 0192512-A 06-DEC-2001;
FEATURES	UNIVERSITY OF DELAWARE (US)
SOURCE	1. 17. /organism="Beta vulgaris" /db_xref="taxon:161934" 5 t
BASE COUNT	6 a 1 c 5 g 5 t
ORIGIN	
QY	1 AGAUACCGUGA 12 : : : Db 4 AGATAACGTGAA 15
Query Match	80.0%; Score 12; DB 6; Length 17;
Best Local Similarity	83.3%; Pred. No. 5.4e+04;
Matches	10; Conservative 2; Mismatches 0;
Indels	0; Gaps 0;
Db	4 AGATAACGTGAA 15
RESULT 3	
AX325566/c	
DEFINITION	Sequence 17/04 from Patent WO0192512.
ACCESSION	AX325566
VERSION	AX325566.1 GI:18096323
KEYWORDS	Beta vulgaris.
SOURCE	Eukaryota; Viridiplanteae; Streptophyta; Embryophyta; Tracheophyta; Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
ORGANISM	Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;
REFERENCE	Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
AUTHORS	Targeted chromosomal genomic alterations in plants using modified
TITLE	single stranded oligonucleotides
JOURNAL	Patent: WO 0192512-A 17/04 06-DEC-2001;
FEATURES	UNIVERSITY OF DELAWARE (US)
SOURCE	1. .17. /organism="Beta vulgaris" /db_xref="taxon:161934" 5 t
BASE COUNT	7 a 1 c 4 g 3 t
ORIGIN	
QY	1 AGAUACCGUGA 12 : : : Db 14 AGATAACGTGAA 3
Query Match	100.0%; Score 12; DB 6; Length 17;
Best Local Similarity	83.3%; Pred. No. 5.4e+04;
Matches	10; Conservative 2; Mismatches 0;
Indels	0; Gaps 0;
RESULT 4	
AX254729/c	
LOCUS	AX254729 20 bp DNA
DEFINITION	Sequence 18 from Patent WO0171027.
ACCESSION	AX254729
VERSION	AX254729.1 GI:16074396
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1. (bases 1 to 20)
AUTHORS	Zohlihoefer, D. and Klein, C.
TITLE	Mirna amplification
JOURNAL	Patent: WO 0171027-A 18 27-SEP-2001;
FEATURES	Micromet AG (DE)
SOURCE	1. .20. /organism="synthetic construct" /db_xref="taxon:32630" 5 t
BASE COUNT	4 a 6 c 5 g 5 t
ORIGIN	
QY	5 ACCUGUAAGAU 15 : : : Db 13 AACGGTGAAT 3
Query Match	73.3%; Score 11; DB 6; Length 20;
Best Local Similarity	81.8%; Pred. No. 2e+05;
Matches	9; Conservative 2; Mismatches 0;
Indels	0; Gaps 0;
Db	13 AACGGTGAAT 3
RESULT 5	
AX255079/c	
LOCUS	AX255079 20 bp DNA
DEFINITION	Sequence 18 from Patent WO0170953.
ACCESSION	AX255079
VERSION	AX255079.1 GI:16074565
KEYWORDS	synthetic construct.
SOURCE	synthetic construct.
ORGANISM	artificial sequences.
REFERENCE	1. (bases 1 to 20)
AUTHORS	Zohlihoefer, D., Bauerle, P., Klein, C. and Neumann, F.J.
TITLE	Identification of modulators of the interferon gamma signaling pathway and their use in restenosis treatment
JOURNAL	Patent: WO 0170953-A 18 27-SEP-2001;
FEATURES	Micromet AG (DE)
SOURCE	1. .20. /organism="synthetic construct" /db_xref="taxon:32630" 5 t
BASE COUNT	4 a 6 c 5 g 5 t
ORIGIN	
QY	5 AACGUGAAGU 15 : : : Db 13 AACGGTGAAT 3
Query Match	73.3%; Score 11; DB 6; Length 20;
Best Local Similarity	81.8%; Pred. No. 2e+05;
Matches	9; Conservative 2; Mismatches 0;
Indels	0; Gaps 0;

RESULT 6
 LOCUS AX296064/C
 DEFINITION Sequence 7826 from Patent WO0179548.
 ACCESSION AX296054
 KEYWORDS synthetic construct.
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE artificial sequences.

AUTHORS Barany, F., Zirvi, M., Gerry, N.P., Favis, R. and Kliman, R.
 TITLE Method of designing addressable array for detection of nucleic acid sequence differences using ligase detection reaction
 JOURNAL Patent: WO 019548-A 7/26 23-OCT-2001;
 CORNELL RESEARCH FOUNDATION, INC. (US)

FEATURES source
 BASE COUNT 1. 20
 ORIGIN Location/Qualifiers
 1. 20
 /organism="synthetic construct"
 /db_xref="taxon:3230"
 /note="Hypothetical Probe Sequence"

Query Match 72.0%; Score 10.8; DB 6; Length 20;
 Best Local Similarity 64.3%; Pred. No. 2.7e+05;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAUAUGUGAGAU 15.
 Db 15 GCTAACGTGAGGAT 2

RESULT 7
 LOCUS AX304787/C
 DEFINITION Sequence 22 from Patent EP1158045.
 ACCESSION AX304787
 VERSION AX304787.1 GI:17644468
 KEYWORDS synthetic construct.
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE artificial sequences.

AUTHORS Schneider, Y.J. and Burteau, N.
 TITLE Culture conditions allowing to modulate the expression of cyp3a4 in hepatocytes
 JOURNAL Patent: EP 1158045-A 22 28-NOV-2001;
 FEATURES source
 BASE COUNT 1. 20
 ORIGIN UNIVERSITE CATHOLIQUE DE LOUVAIN (BE)
 /organism="synthetic construct"
 /db_xref="taxon:3230"
 /note="Oligonucleotide" 7 t

Query Match 72.0%; Score 10.8; DB 6; Length 20;
 Best Local Similarity 64.3%; Pred. No. 2.7e+05;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAUAUGUGAGAU 15.
 Db 20 GCTAACGTGAGGAT 7

RESULT 8
 LOCUS AX349237/C
 DEFINITION Sequence 21 from Patent WO202810.
 ACCESSION AX349237

Query Match 69.3%; Score 10.8; DB 6; Length 20;
 Best Local Similarity 64.3%; Pred. No. 2.7e+05;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAUAUGUGAGAU 15.
 Db 20 GCTAACGTGAGGAT 7

RESULT 9
 LOCUS AX272471/C
 DEFINITION Sequence 40 from Patent WO0162911.
 ACCESSION AX272471
 VERSION AX272471.1 GI:16545208
 KEYWORDS SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE AUTHORS
 1 Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and Ellis, J.H.
 TITLE JOURNAL Method and reagent for the inhibition of grid Patent: WO 0162911-A 40 30-AUG-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
 FEATURES source
 BASE COUNT 1. 17
 ORIGIN /organism="Homo sapiens"
 /db_xref="taxon:9606"
 6 a 5 c 2 g 4 t

Query Match 69.3%; Score 10.4; DB 6; Length 17;
 Best Local Similarity 66.7%; Pred. No. 4.6e+05;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 UAAUGUGAGAU 15.
 Db 16 TAACGTGAGCT 5

RESULT 10
 LOCUS AX272472/C
 DEFINITION Sequence 41 from Patent WO0162911.
 ACCESSION AX272472
 VERSION AX272472.1 GI:16545209
 KEYWORDS SOURCE
 human.
 Homo sapiens
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1
 AUTHORS Jarvis, T., von Carlowitz, I., McSwiggen, J.A., Hamblin, P.A. and
 Ellis, J.H.
 TITLE Method and reagent for the inhibition of grid
 JOURNAL Patent: WO 0162911-A 30-AUG-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
 FEATURES source
 BASE COUNT 7 a
 ORIGIN /db_xref="taxon:9606"
 Query Match 1
 Best Local Similarity 69.3%; Score 10.4; DB 6; Length 17;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 4 UAACGUGAAU 15
 Db 15 TAACGTGAGCT 4
 RESULT 11
 AX272653/C
 LOCUS AX272653
 DEFINITION Sequence 222 from Patent WO0162911.
 ACCESSION AX272653
 VERSION AX272653.1
 KEYWORDS human.
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Cetartiodactyla; Hominoidea; Homo.
 REFERENCE 1
 AUTHORS Jarvis, T., von Carlowitz, I., McSwiggen, J.A., Hamblin, P.A. and
 Ellis, J.H.
 TITLE Method and reagent for the inhibition of grid
 JOURNAL Patent: WO 0162911-A 222 30-AUG-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
 FEATURES source
 BASE COUNT 6 a
 ORIGIN /db_xref="taxon:9606"
 Query Match 1
 Best Local Similarity 69.3%; Score 10.4; DB 6; Length 17;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 4 UAACGUGAAU 15
 Db 17 TAACGTGAGCT 6
 RESULT 12
 AX272654/C
 LOCUS AX272654
 DEFINITION Sequence 223 from Patent WO0162911.
 ACCESSION AX272654
 VERSION AX272654.1
 KEYWORDS human.
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Cetartiodactyla; Hominoidea; Homo.
 REFERENCE 1
 AUTHORS Jarvis, T., von Carlowitz, I., McSwiggen, J.A., Hamblin, P.A. and
 Ellis, J.H.
 TITLE Method and reagent for the inhibition of grid
 JOURNAL Patent: WO 0162911-A 223 30-AUG-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
 FEATURES source
 BASE COUNT 7 a
 ORIGIN /db_xref="taxon:9606"
 Query Match 1
 Best Local Similarity 69.3%; Score 10.4; DB 6; Length 17;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 4 UAACGUGAAU 15
 Db 14 TAACGTGAGCT 3
 RESULT 13
 AX272993/C
 LOCUS AX272993
 DEFINITION Sequence 562 from Patent WO0162911.
 ACCESSION AX272993
 VERSION AX272993.1
 KEYWORDS human.
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Cetartiodactyla; Hominoidea; Homo.
 REFERENCE 1
 AUTHORS Jarvis, T., von Carlowitz, I., McSwiggen, J.A., Hamblin, P.A. and
 Ellis, J.H.
 TITLE Method and reagent for the inhibition of grid
 JOURNAL Patent: WO 0162911-A 562 30-AUG-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
 FEATURES source
 BASE COUNT 5 a
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 Query Match 1
 Best Local Similarity 69.3%; Score 10.4; DB 6; Length 17;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 4 UAACGUGAAU 15
 Db 12 TAACGTGAGCT 1
 RESULT 14
 AX299883/C
 LOCUS AX299883
 DEFINITION Sequence 24 from Patent WO0183790.
 ACCESSION AX299883
 VERSION AX299883.1
 KEYWORDS synthetic construct.
 SOURCE
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Conner, T.W., Dubois, R., Malven, M. and Masucci, J.D.
 TITLE Plant regulatory sequences for selective control of gene expression
 JOURNAL Patent: WO 0183790-A 24 30-NOV-2001;
 Monsanto Technology LLC (US)
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 ORIGIN /note="Fully Synthesized Primer"
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		:								
Db	16	GACACCTGAG	5							
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DEFINITION	Sequence 1699 from Patent WO0192512.		DNA							
ACCESSION	AX325561									
VERSION	AX325561.1									
KEYWORDS										
SOURCE	Beta vulgaris									
ORGANISM	Beta vulgaris									
REFERENCE	1									
AUTHORS	Kmiec, E.B., Camper, H.B., Rice, M.C. and Kim, J.									
TITLE	Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides									
JOURNAL	Patent: WO 0192512-A 1699 05-DEC-2001;									
FEATURES	UNIVERSITY OF DELAWARE (US)									
source	Location/Qualifiers									
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Best Local Similarity	75.0%		Pred. No. 4.6e-05;							
Matches	9;	Conservative	2;	Mismatches 1;	Indels 0;	Gaps 0;				
QY	1	AGAUACCUGAAG	12							
	: 1:									
Db	4	AGATAATGTGAA	15							

Search completed: May 22, 2003, 19:36:39
 Job time : 876.364 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 16:52:30 ; Search time 146.364 Seconds
(without alignments)

230.795 Million cell updates/sec

Title: US-09-780-929-97
Perfect score: 15
Sequence: 1 agauaaacgaaagau 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters:

1367302

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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	c	44	10	66.7	13	23	ABC1636
	c	45	10	66.7	13	23	ABC19637

ALIGNMENTS

RESULT	ID	NAME	TYPE	SEQUENCE	SCORE	SEGMENT	DESCRIPTION
1	AAS12347	AAS12347 standard; DNA; 15 BP.	XX				
2	AAS12347;	AC	XX				
3		XX	XX				
4		DT	21-NOV-2001 { first entry }				
5		DE	DNA encoding deoxyribozyme #7.				
6		XX	Deoxyribozyme; cytostatic; endonuclease; RNA cleavage; DNA cleavage; gene therapy; plant; fungus; bacteria; mammal; ribozyme; ss.				
7		XX	Synthetic.				
8		XX	OS				
9		PN	W0200159102-A2.				
10		FD	16-AUG-2001.				
11		XX	PP	08-FEB-2001; 2001WO-US04223.			
12		XX	PR	08-FEB-2000; 2000US-0181360.			
13		XX	PR	31-MAR-2000; 2000US-0193646.			
14		PA	(RIBO-) RIBOZYME PHARM INC.				
15		PA	(UVYA-) UNIV YALE.				
16		PI	Breaker R, Beigelman L, Emilsson G;				
17		XX	WPI; 2001-536526/59.				
18		XX	New nucleic acids with endonuclease activity, such as ribozymes and				
19		PCR primer used to					

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Length	DB ID	Description
1	15	100.0	15 22	AS12347
2	12	80.0	17 20	AAA18478
3	12	80.0	17 24	ABK26543
4	12	80.0	17 24	ABK20344
5	11.4	76.0	13 23	ABF31424
6	11.4	76.0	13 23	ABF31425
7	11.4	76.0	13 23	ABF76054
8	11.4	76.0	13 23	ABF76055
9	11.4	76.0	20 20	AAZ0321

PT nucleozymes, for modulating gene expression in a plant, mammalian,
 PT bacterial or fungal cell
 XX
 PS Claim 49; Page 77; 96pp; English.

CC The invention relates to nucleic acid molecules with endonuclease
 activity, which are particularly useful for cleavage of RNA or DNA.
 CC The nucleic acids are used in a pharmaceutical composition and are used
 to modulate expression of a gene in a plant, mammalian, bacterial or
 fungal cell. They are used to cleave a separate nucleic acid, preferably
 RNA. The nucleic acids are used to inhibit gene expression and/or cell
 proliferation, and can be used to treat a disease or condition. More
 than one nucleic acid can be independently targeted to the same or
 different sites in a cell. The nucleic acids may be used to study DNA.
 CC The modifications to the nucleic acids optimises their catalytic activity
 and can maintain or enhance their activity. They exhibit a high degree
 of specificity for RNA. The present sequence represents the coding
 CC sequence of deoxyribozyme #7 used in the method of the invention.
 XX Sequence 15 BP; 7 A; 1 C; 4 G; 3 U; 0 other;
 SQ

Query Match	100.0%	Score	15	DB	22	Length	15
Best Local Similarity	100.0%	Pred.	No.	71			
Matches	15	Conservative	0	Mismatches	0	Indels	0
Qy	1 AGAUACCGUGAACU 15						
Db	1 AGAUACCGUGAGAU 15						

RESULT 2

DT	AAA18478	ID	AAA18478	Standard;	RNA:	17	BP.
XX		AC	AAA18478;				
XX							

DE Human TIE-2 substrate sequence SEQ ID NO:1704.

XX	KW Human;	KW aryl hydrocarbon nuclear transport;	KW ARNT; TIE-2; angiogenesis;
KW hammerhead ribozyme;	KW integrin alpha 5 subunit; integrin subunit beta 3; hairpin ribozyme;		
KW ophthalmologic; antiinflammatory; antidiabetic;	KW angiogenic factor; cytosstatic; antidiabetic; ARND;		
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;	KW age related macular degeneration; inflammation; neovascular glaucoma;		
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;	KW tiberos scleriosis; pot-wine stain; Sturge Weber syndrome;		
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.	KW Osmosis.		
OS Homo sapiens.			
PN WO9950403-A2.			
PD 07-OCT-1999.			
XX 24-MAR-1999;	99WO-US06507.		
PR 27-MAR-1998;	98US-0079678.		
XX			
PA (RIBO-) RIBOZYME PHARM INC.			
XX			
PI RAVCO PA,	Roberts E, Jarvis T, Coeshott C, McSwigan JA;		
XX			
DR WPT; 1999-591315/50.			
XX			
PT Novel ribozymes for modulating the synthesis, expression and/or			
PT stability of an mRNA encoding an angiogenic factors			
XX			
PS Claim 56; Page 97; 305pp; English.			
XX			
CC The present invention describes enzymatic nucleic acid molecules with			
CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl			

CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 corresponding target sequences; AAA1685 to AAA1835 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA2086
 and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AA19223 to AAA20361 and AAA21501 to AAA19595 represent ribozyme
 sequences for integrin alpha 6 subunit, and AAA20562 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA2363 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA2262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tubercous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 XX Sequence 17 BP; 7 A; 2 C; 6 G; 2 U; 0 other;
 SQ

Query Match	80.0%	Score	12	DB	20	Length	17
Best Local Similarity	100.0%	Pred.	No.	3.2e+03			
Matches	12	Conservative	0	Mismatches	0	Indels	0
Qy	1 AGAUACCGUGAA 12						
Db	5 AGAUACCGUGAA 16						

RESULT 3

DT	ABK26343	ID	ABK26343	standard;	DNA;	17	BP.
XX	AC	ABK26343;					
XX							

DE Increased starch production genome altering oligonucleotide #195.

XX	KW chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW O-methyl modification; LNA modification; phosphorothioate linkage;	
KW KW repair; DNA alteration; environmental tolerance; hygromycin B;	
KW amino acid over production; herbicide resistance; glyphosate resistance;	
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;	
KW porphyrin herbicide resistance; triazine resistance; disease resistance;	
KW modified oil production; modified starch production; waxy starch;	
KW altered floral morphology; male-sterile plant; albino mutant;	
KW modified fatty acid content; reduced palmitate production; albino plant;	
KW increased stearate production; reduced linolenic acid production;	
KW photosynthetic process.	
OS Beta vulgaris.	
OS Synthetic.	
XX	
PN WO200192512-A2.	
XX	
PD 06-DEC-2001.	
XX	
PF 01-JUN-2001; 2001WO-US17672.	
XX	
PR 01-JUN-2000; 2000US-208338P.	
PR 30-OCT-2000; 2000US-244989P.	
PR 27-MAR-2001; 2001US-0818875.	
XX	
PA (UYDE) UNIV DELAWARE.	

PD 18-OCT-2001.
 XX
 PP 06-APR-2001; 2001WO-IB00713.
 XX
 PR 07-APR-2000; 2000DE-1019173.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-65177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 designed to detect single nucleotide polymorphisms and cytosine
 methylation status -
 PT
 XX
 PS Claim 1; SEQ ID 131422; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 range of diseases including immune system, gastrointestinal, respiratory,
 central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 ABC0010-ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and
 ABI0010-ABI203 represent the oligomers described in the invention.
 NOTE: The sequence data for this patent did not form part of the printed
 specification, but was obtained in electronic format from WIPO at
 ftp://wipo.int/pub/published_pct_sequences.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 range of diseases including immune system, gastrointestinal, respiratory,
 central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 ABC0010-ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and
 ABI0010-ABI203 represent the oligomers described in the invention.
 NOTE: The sequence data for this patent did not form part of the printed
 specification, but was obtained in electronic format from WIPO at
 ftp://wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 13 BP; 5 A; 1 C; 5 G; 2 T; 0 other;
 Query Match 76.0%; Score 11.4; DB 23; Length 13;
 Best Local Similarity 76.9%; Pred. No. 6.8e+03;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 AGAUAAACGGAG 13
 |||:||||:|||
 Db 1 AGATAACGTGAGG 13
 13 AGATACCGTGGAG 1
 RESULT 6
 ABF31425/C
 ID ABF31425 standard; DNA; 13 BP.
 XX
 AC ABF31425;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 131422 for detecting SNP TSC0032802.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic;
 KW Homo sapiens.
 OS Homo sapiens.
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PT 06-APR-2001; 2001WO-IB00713.
 XX
 PR 07-APR-2000; 2000DE-1019173.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-65177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 designed to detect single nucleotide polymorphisms and cytosine
 methylation status -
 PT
 XX
 PS Claim 1; SEQ ID 176051; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 range of diseases including immune system, gastrointestinal, respiratory,
 central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 ABC0010-ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and

CC AB100010-AB182073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at:
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 6 A; 1 C; 5 G; 1 T; 0 other;
 SQ Query Match 76.0%; Score 11.4; DB 23; Length 13;
 Best Local Similarity 84.6%; Pred. No. 6.8e+03;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GAURACGUGAAGA 14
 Db 1 GAGAACCGTGAGA 13
 ||||||:|||||
 RESULT 8
 ABF76055/C
 ID ABF76055 standard; DNA; 13 BP.
 XX AC ABF76055;
 XX DE Oligonucleotide SEQ ID NO 176052 for detecting SNP TSC0043704.
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; RNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX PN WO20017384-A2.
 XX PR 22-FEB-2002 (first entry)
 XX DE 18-OCT-2001.
 XX PR 06-APR-2001; 2001WO-IB00713.
 XX PR 07-APR-2000; 2000DE-1019173.
 XX PA (EPIG-) EPPGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 DR XX WPI; 2001-65177/75.
 PR XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status
 XX PS Claim 1; SEQ ID 176052; 29pp + Sequence Listing; German.
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP). The
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. The
 CC ABC0010-ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and
 CC ABT0010-ABT82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at:
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 13 BP; 1 A; 5 C; 1 G; 6 T; 0 other;
 CC Query Match 76.0%; Score 11.4; DB 20; Length 20;
 CC Best Local Similarity 69.2%; Pred. No. 6.9e+03;
 CC Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 3 AUURACGUGACAG 15
 Db 2 ATAACGGGAGAT 14
 ||||:|||||
 RESULT 10
 AB125946/C
 ID AB125946 standard; DNA; 12 BP.
 XX AC AB125946;
 XX DT 22-FEB-2002 (first entry)
 XX PN 2 GAURACGUGAAGA 14
 ||||||:|||||

DE Oligonucleotide primer SEQ ID NO 325919 for detecting SNP TSC0032801.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-1B00713.
 XX
 PR 07-APR-2000; 2000DE-1019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A., Piepenbrock C., Berlin K;
 DR XX
 PR Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX
 PS Claim 1; SEQ ID 378713; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-RBH9989 and
 CC AB100010-AB18203 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 12 BP; 2 A; 4 C; 1 G; 5 T; 0 other;
 XX
 Query Match 73.3%; Score 11; DB 23; Length 12;
 Best Local Similarity 81.8%; Pred. No. 1.1e+04;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 3 AUUACUGAG 13
 DB 1 ATAACGTGAAG 11
 RESULT 12
 ABB60400
 ID ABB60400 standard; DNA; 13 BP.
 XX
 AC ABB60400;
 XX
 DT 22-FEB-2002 (First entry)
 XX
 DE Oligonucleotide SEQ ID NO 160397 for detecting SNP TSC0040381.
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-1B00713.
 XX
 PR 07-APR-2000; 2000DE-1019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A., Piepenbrock C., Berlin K;
 DR XX
 PR WPI; 2001-651717/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 XX
 methylation status -

XX . Claim 1; SEQ ID 160397; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation.

CC ABC0010-ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and CC ABI10010-ABI8203 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at CC ftp://wipo.int/pub/published_pct_sequences.

CC XX SQ Sequence 13 BP; 6 A; 1 C; 3 G; 3 T; 0 other;

Query Match 73.3%; Score 11; DB 23; Length 13;

Best Local Similarity 81.8%; Pred. No. 1.1e+04;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0

Oy 3 AUUACCGUAAG 13
|:||||:||||:
Db 2 ATAACGTGAG 12

RESULT 13

ABF60401/C
ID ABF60401 standard; DNA; 13 BP.

XX AC ABF64401;
XX DT 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 160398 for detecting SNP TSC0040381.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic

XX OS Homo sapiens.
XX PN WO2017734-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-TB00713.

XX PR 07-ARR-2000; 2000DE-1019473.

PA (EPIC-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine PT methylation status

XX PS Claim 1; SEQ ID 160398; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC0010-ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI10010-ABI8203 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

CC ftp wipo int/pub/published_pct_sequences.
 XX
 SQ Sequence 13 BP; 3 A; 3 C; 1 G; 6 T; 0 other;
 Query Match 73.3%; Score 11; DB 23; Length 13;
 Best Local Similarity 81.8%; Pred. No. 1.1e+04; Indels 0;
 Matches 9; Conservative 2; Mismatches 0; Gaps 0;
 QY 3 AUAACGUGAG 13
 I:||||:|||
 Db 12 ATAACGTGAA 2
 RESULT 14
 AAI6878/C
 ID AAI6878 standard; DNA; 20 BP.
 XX
 AC AAI6878;
 XX DT 07-JAN-2002 (first entry)
 DE Nucleotide sequence of primer seq Id No. 18.
 KW Nucleic acid amplification; hybridization assay; interaction assay;
 expression cloning; PCR primer; ss.
 XX OS Synthetic.
 XX PA WO200171027-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-EP03311.
 XX PR 24-MAR-2000; 2000EP-0106450.
 XX PA (MICR-) MICROMET AG.
 XX PI zohlinhoefer D, Klein C;
 XX DR WPI; 2001-611514/70.
 PT A method for the amplification of mRNA from a sample, e.g. for the
 preparation of in vitro surrogates for pathologically modified cells or
 tissues -
 PS Examples; Page 168; 170pp; English.
 XX
 CC The invention provides a novel method for the amplification of mRNA from
 a sample. The method comprises (1) generating cDNA from polyadenylated
 RNA employing at least one primer hybridizing to the polyadenylated RNA and
 comprising a 5' poly(C) or a 5' poly(G) flank; (2) (either): (a)
 (optionally): (1) (if present) removing non-hybridized, surplus primer(s)
 and/or surplus dNTPs; (1)(3), tailing of the generated cDNA with a poly
 (G) tail when in step (1) primer(s) comprising a 5' poly(C) flank was/
 were employed or a poly(C) tail when in step (1) primer(s) comprising a
 5', poly(G) flank was/were employed; or (b) (optionally) 3, tailing of the
 generated cDNA with a poly(G) tail when in step (1) primer(s) comprising
 a 5', poly(C) Flank was/were employed or a poly(C) tail when in step (1)
 primer(s) comprising a 5' poly(G) Flank was/were employed using an RNA-
 ligase, irrespective of the presence or absence of surplus primer(s) and
 /or surplus dNTPs; and (3) amplifying the tailed cDNA with a primer
 hybridizing to the tails generated in step (2a) or (2b). The amplified
 cDNA obtained may be used for in vitro and/or in vivo expression and
 preparation of mRNA transcripts (which may then be used in hybridization
 assays (comprising hybridization to oligonucleotide arrays, cDNA arrays
 and/or DNA arrays) and/or interaction assays (comprising interactions
 with carbohydrates, lectins, ribozymes, proteins, peptides, antibodies
 and/or aptamers) and for sequence specific PCR, cDNA cloning,
 subtractive hybridization cloning and/or expression cloning. Sequences
 AAT6876-890 represent primers used in the method of the invention.
 SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match 73.3%; Score 11; DB 22; Length 20;
 Best Local Similarity 81.8%; Pred. No. 1.2e+04;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Search completed: May 22, 2003, 19:04:24
 Job time : 148.364 secs

Qy	5	AACGUGAGAU	15
		: :	
Db	13	AACGTGAGAT	3

RESULT 15

AAD19670/c

ID AAD19670 standard; DNA; 20 BP.

XX

AC AAD19670;

XX

DT 18-DEC-2001 (first entry)

XX

DE Desmin PCR primer #2 related to the invention.
 XX
 KW Inhibitor; interferon-gamma; IFN-gamma signalling pathway; therapy;
 KW restenosis; coronary artery; carotid artery; femoralis artery;
 KW aorta-coronary vein bypass; arterial bypass; venous bypass;
 KW balloon angioplasty; stent implantation; vasotropic; PCR primer; ss.
 OS Unidentified.

XX

PN WO200170953-A2.

XX

PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-EP03312.
 XX
 PR 24-MAR-2000; 2000EP-0106468.
 XX
 PA (MICR-) MICROMET AG.
 XX
 PI Zohlnhoefer D, Baeuerle P, Klein C, Neumann F;
 DR WPI; 2001-616404/71.
 XX
 XX
 PT Use of an inhibitor of the interferon-gamma signaling pathway for
 PT preparation of a pharmaceutical composition useful in the treatment or
 PT prevention of restenosis -
 XX
 PS Example 5; Page 55; 151pp; English.

The present invention relates to the use of an inhibitor of the interferon-gamma (IFN-gamma) signalling pathway for the preparation of a pharmaceutical composition for the treatment or prevention of restenosis. The inhibitor is useful for the preparation of a pharmaceutical composition useful in treating or preventing restenosis which include restenosis of coronary arteries, carotid arteries, femoralis arteries, aorta-coronary vein bypass, arterial bypass, and/or venous bypass; and restenotic modification, where prevention of restenotic modification is done before, during and/or after balloon angioplasty and/or stent implantation and the restenosis or restenotic modification is in-stent restenosis; and for treating and preventing restenosis in a subject preferably human. The present sequence is a desmin PCR primer which is used in aberrant gene expression in human restenotic tissue used in the exemplification of the invention. Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match 73.3%; Score 11; DB 22; Length 20;
 Best Local Similarity 81.8%; Pred. No. 1.2e+04;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy	5	AACGUGAGAU	15
		: :	
Db	13	AACGTGAGAT	3

		Plate: 0553 row: A column: 08
		Seq primer: CGTGTAAACGACGCCAGT
		Class: plasmid ends
		High quality sequence stop: 19.
FEATURES	source	Location/Qualifiers
		1. .19
		/organism="Mus musculus"
		/strain="C57BL/6J"
		/db_xref="taxon:10090"
		/clone="UUGC1M025A08"
		/clone_lib="Mouse 10kb plasmid UUGC1M library"
		/sex="Male"
		/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
		/note="Vector: PWD42N; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnare/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732149 AF129022.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT	11 a 2 c	3 g 3 t
ORIGIN		
		Query Match Score 10.2; DB 17; Length 19;
	Best Local Similarity 66.7%; Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;	
QY	1 AGAACGUGAAGAU 15	
Db	3 AAAAACGAGAAAT 17	
RESULT 2		
LOCUS	A2465132	19 bp DNA linear GSS 04-OCT-2000
DEFINITION	IM0274D4R mouse 10kb plasmid UUGC1M library mus musculus genomic clone UUGC1M0274D24 R, DNA sequence.	
ACCESSION	A2465132	
VERSION	A2465132.1	GI:10623257
KEYWORDS	GSS	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.	
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.	
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts	
JOURNAL	Unpublished (2000)	
COMMENT	Contact: Robert B. Weiss	
	University of Utah Genome Center	
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA	
	Tel: 801 585 5606	
	Fax: 801 585 7177	
	Email: daunne@genetics.utah.edu	
	Insert Length: 10000	Std Error: 0.00
FEATURES	source	Location/Qualifiers
		1. .19
		/organism="Mus musculus"
		/strain="C57BL/6J"
		/db_xref="taxon:10090"
		/clone="UUGC1M0274D24"
		/clone_lib="Mouse 10kb plasmid UUGC1M library"
		/sex="Male"
		/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
		/note="Vector: PWD42N; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnare/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732149 AF129022.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT	3 a 3 c	4 g 9 t
ORIGIN		
		Query Match Score 10.2; DB 17; Length 19;
	Best Local Similarity 58.7%; Matches 9;保守型 75.0%; Mismatches 1; Indels 0; Gaps 0;	
QY	3 AUUACGUGAAGA 14	
Db	12 AAAACGIGAAA 1	
RESULT 3		
LOCUS	A2603744	19 bp DNA linear GSS 13-DEC-2000
DEFINITION	IM0423E15F mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0423E15 F, DNA sequence.	
ACCESSION	AZ603744	
VERSION	A2603744.1	GI:11725934
KEYWORDS	GSS	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.	
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.	
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts	
JOURNAL	Unpublished (2000)	
COMMENT	Contact: Robert B. Weiss	
	University of Utah Genome Center	
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA	
	Tel: 801 585 5606	
	Fax: 801 585 7177	
	Email: daunne@genetics.utah.edu	
	Insert Length: 10000	Std Error: 0.00

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold ("Stratagene") cells and selected for ampicillin resistance."

BASE COUNT 7 a 4 c 3 g 6 t
ORIGIN

Query Match 56.0%; Score 8.4; DB 17; Length 20;
Best Local Similarity 70.0%; Pred. No. 7.6e+05; 1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 3 AUAGCGUGA 12
Db 9 ATGACGTGAA 18

RESULT 6

C21102/c
LOCUS C21102 19 bp mRNA linear EST 23-OCT-1996

DEFINITION HUMDS002625 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA

SEQUENCE sequence.

ACCESSION C21102

VERSION C21102.1 GI:1622212

KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb GSS.

TITLE house mouse.

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb GSS.

TITLE house mouse.

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb GSS.

TITLE house mouse.

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb GSS.

TITLE house mouse.

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb GSS.

TITLE house mouse.

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb GSS.

TITLE house mouse.

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb GSS.

FEATURES Location/Qualifiers
source
1. .19
/organism="Homo sapiens"
/clone_id="Human adult (K.Okubo)"
/db_xref="taxon:9606"
/sex="Male"
/label host="E. Coli strain XL10-gold, λ -resistant, F-"
/note="Vector: pMD42Nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (91147321141gBAF129072-1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold ("Stratagene") cells and selected for ampicillin resistance."

BASE COUNT 4 a 5 c 1 g 8 t 1 others

ORIGIN

Query Match 54.7%; Score 8.2; DB 14; Length 19;
Best Local Similarity 53.8%; Pred. No. 9.5e+05; 1;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 AUAGCGUGAAGU 15
Db 14. ATGACGTGAA 2

BASE COUNT 5 a 1 c 8 g 5 t

ORIGIN

Query Match 54.7%; Score 8.2; DB 17; Length 19;
Best Local Similarity 69.2%; Pred. No. 9.5e+05; 1;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAUAGCGUGAAGA 14
Db 7 GAGAACTTGTATGA 19

RESULT 7
A2436629

RESULT 8
A2658282/c

LOCUS	AZ345449	19 bp	DNA	linear	GSS 29-SEP-2000	LOCUS	AZ345511	19 bp	DNA	linear	GSS 29-SEP-2000	
DEFINITION	IM0080108F Mouse 10kb Plasmid UGCLM library					DEFINITION	IM0080101F Mouse 10kb plasmid UGCLM library					
ACCESSION	AZ345449					ACCESSION	AZ345511					
VERSION	AZ345449.1					VERSION	AZ345511.1					
KEYWORDS	GSS,					KEYWORDS	GSS,					
SOURCE	house mouse.					SOURCE	house mouse.					
ORGANISM	Mus musculus					ORGANISM	Mus musculus					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
REFERENCE	1 (bases 1 to 19)					REFERENCE	1 (bases 1 to 19)					
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Maenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederausen,A.					AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,' Islam,H., Longacre,S., Mahmoud,M., Maenen,E., Pedersen,T.,' Reilly,M., Rose,M.,' Rose,R., Stokes,R., Tingey,A.,' von Niederausen,A.					
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts					TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts					
JOURNAL	Unpublished (2000)					JOURNAL	Unpublished (2000)					
COMMENT	Contact: Robert B. Weiss					COMMENT	Contact: Robert B. Weiss					
CONTACT	University of Utah Genome Center					CONTACT	University of Utah Genome Center					
UNPUBLISHED	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT					UNPUBLISHED	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT					
TEL	801 585 5606					TEL	801 585 5606					
FAX	801 585 7177					FAX	801 585 7177					
EMAIL	dunne@genetics.utah.edu					EMAIL	dunne@genetics.utah.edu					
INSERT LENGTH	10000	Std Error:	0.00			INSERT LENGTH	10000	Std Error:	0.00			
PLATE	0080	row:	I	column:	08	PLATE	0080	row:	J	column:	01	
SEQ PRIMER	C GTT G T C T A A A G G A C G G C C A G T					SEQ PRIMER	C GTT G T C T A A A G G A C G G C C A G T					
CLASS	Plasmid ends					CLASS	plasmid ends					
FEATURES	High quality sequence stop: 19.					FEATURES	High quality sequence stop: 19.					
SOURCE	Location/Qualifiers					SOURCE	Location/Qualifiers					
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/strain="C57BL/6J"						/strain="C57BL/6J"						
/db_xref="taxon:10090"						/db_xref="taxon:10090"						
/clone="UGCLM0080108"						/clone="UGCLM0080108"						
/clone_id="Mouse 10kb plasmid UGCLM library"						/clone_id="Mouse 10kb plasmid UGCLM library"						
/sex="Male"						/sex="Male"						
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-						/lab_host="E. coli strain XL10-Gold, T1-resistant, F-						
/note="Vector: Pwd42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource						/note="Vector: Pwd42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource						
(http://www.jax.org/resources/documents/dshares/). The DNA was hydrodynamically sheared by repeated passage through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of Pwd42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."						(http://www.jax.org/resources/documents/dshares/). The DNA was hydrodynamically sheared by repeated passage through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of Pwd42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."						
BASE COUNT	4 a 9 c 0 g 6 t					BASE COUNT	4 a 9 c 0 g 6 t					
ORIGIN						ORIGIN						
QUERY MATCH	52.0%; Score 7.8; DB 17; Length 19;					QUERY MATCH	52.0%; Score 7.8; DB 17; Length 19;					
BEST LOCAL SIMILARITY	63.6%	PRED. NO.	1.6e+06;			BEST LOCAL SIMILARITY	63.6%	PRED. NO.	1.6e+06;			
MATCHES	7;	CONSERVATIVE	2;	MISMATCHES	2;	MATCHES	7;	CONSERVATIVE	2;	MISMATCHES	2;	
QY	2 GAUACCGUGAA 12	INDELS	0;	GAPS	0;	QY	2 GAUACCGUGAA 12	INDELS	0;	GAPS	0;	
DB	13 GGTAGGTGAA 3					DB	13 GGTAGGTGAA 3					
RESULT	13					RESULT	14					
	AZ345511/c						AZ345536/c					

LOCUS AZ345536 19 bp DEFINITION AZ345536 Mouse 10kb plasmid UGGC1M library Mus musculus genomic
 ACCESSION AZ345536
 VERSION AZ345536.1 GI:10424773
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 Plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0080 row: O column: 06
 Seq primer: CGTGTGTAACACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES source
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 /strain="C57BL/6J"
 /clone_id="Mouse 10kb plasmid UGGC1M library"
 /db_xref="taxon:10090"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, λ -resistant, F-"
 /note="Vector: PWD4Inv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://wwwjax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor Oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gil47321149bAF129072.1), a copy-number
 inducible derivative of plasmid RI. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT
 ORIGIN 4 a 9 c 0 g 6 t

LOCUS AZ345572 19 bp DEFINITION AZ345572 Mouse 10kb plasmid UGGC1M library Mus musculus genomic
 ACCESSION AZ345572
 VERSION AZ345572.1 GI:10424809
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 Plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0080 row: J column: 17
 Seq primer: CGTTGAATAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES source
 1..19
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /clone_id="Mouse 10kb plasmid UGGC1M library"
 /db_xref="taxon:10090"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, λ -resistant, F-"
 /note="Vector: PWD4Inv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
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 (<http://wwwjax.org/resources/documents/dnares/>). The DNA
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 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT
 ORIGIN 4 a 9 c 0 g 6 t

Query Match 52.0%; Score 7.8; DB 17; Length 19;
 Best Local Similarity 63.6%; Pred. No. 1.6e+06;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 GAUAGCUGAA 12
 | : | : |||
 DB 13 GGTAAGGTGA 3

RESULT 15
 A2345572/c

Search completed: May 22, 2003, 20:17:01
 Job time : 1100.18 secs

Sun May 25 14:49:07 2003

us-09-780-929-97.szlm20.rst

GenCore version 5.1.4-p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 18:55:07 ; Search time 32.2727 Seconds
(without alignments)

142.540 Million cell updates/sec

Title: US-09-780-929-97

Perfect score: 15

Sequence: 1 agauaaccgugaaagau 15

Scoring table: IDENTITY_NUC

Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 247290

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Listing first 45 summaries

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfileseq1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	10.8	72.0	20	4	US-09-780-175-22		Sequence 22, Appli
C 3	10.2	68.0	15	1	US-08-182-968A-447		Sequence 447, Appli
C 4	10.2	68.0	15	2	US-08-774-306A-447		Sequence 447, Appli
C 5	10.2	68.0	15	3	US-09-064-150A-447		Sequence 447, Appli
C 6	10.2	68.0	19	1	US-08-580-031-29		Sequence 447, Appli
C 7	10	66.7	20	4	US-09-80-175-50		Sequence 50, Appli
C 8	9.8	65.3	17	1	US-09-738-300-1325		Sequence 1325, Appli
C 9	9.8	65.3	18	3	US-09-205-143-70		Sequence 70, Appli
C 10	9.8	65.3	20	4	US-09-561-497-82		Sequence 82, Appli
C 11	9.8	65.3	20	4	US-09-841-630-63		Sequence 63, Appli
C 12	9.6	64.0	17	1	US-08-305-745-5		Sequence 5, Appli
C 13	9.6	64.0	17	4	US-08-482-388-5		Sequence 5, Appli
C 14	9.6	64.0	17	4	US-08-474-852-5		Sequence 5, Appli
C 15	9.6	64.0	17	4	US-09-166-205B-5		Sequence 5, Appli
C 16	9.6	64.0	17	5	PCT-US94-02620-5		RESULT 2
C 17	9.4	62.7	12	3	US-08-781-891-67		US-09-780-175-22/C
C 18	9.4	62.7	15	2	US-08-585-684B-1349		Sequence 22, Application US/09780175
C 19	9.4	62.7	15	2	US-08-583-684B-1350		Sequence 1349, Application US/09780175
C 20	9.4	62.7	15	4	US-09-038-071-1349		Sequence 1350, Application US/09780175
C 21	9.4	62.7	15	4	US-09-038-071-1349		Sequence 1349, Application US/09780175
C 22	9.4	62.7	15	4	US-09-038-073-1350		Sequence 1350, Application US/09780175
C 23	9.4	62.7	15	4	US-09-081-646-221		Sequence 221, Application US/09780175
C 24	9.4	62.7	17	2	US-08-173-482C-69		Sequence 69, Application US/09780175
C 25	9.4	62.7	18	2	US-09-213-768-43		Sequence 43, Application US/09780175
C 26	9.4	62.7	18	3	US-09-358-381-29		Sequence 29, Application US/09780175
C 27	9.4	62.7	18	3	US-09-061-195-4		Sequence 4, Application US/09780175

ALIGNMENTS

C 28	9.4	62.7	18	4	US-09-577-902-29	Sequence 29, Appli
C 29	9.4	62.7	20	3	US-09-436-605-16	Sequence 16, Appli
C 30	9.4	62.7	20	4	US-09-205-283-10	Sequence 10, Appli
C 31	9.4	62.7	20	4	US-09-280-805-112	Sequence 112, Appli
C 32	9.4	62.7	20	4	US-09-593-711A-240	Sequence 240, Appli
C 33	9.4	62.7	20	4	US-09-593-711A-241	Sequence 241, Appli
C 34	9.4	62.7	20	4	US-09-588-095-63	Sequence 63, Appli
C 35	9.4	62.7	20	4	US-09-517-467B-60	Sequence 60, Appli
C 36	9.2	61.3	15	4	US-09-081-646-75	Sequence 75, Appli
C 37	9.2	61.3	15	4	US-09-164-828	Sequence 828, Appli
C 38	9.2	61.3	17	1	US-08-758-306-1323	Sequence 1323, Appli
C 39	9.2	61.3	18	2	US-09-205-204-24	Sequence 24, Appli
C 40	9.2	61.3	18	3	US-09-255-888-10	Sequence 10, Appli
C 41	9.2	61.3	18	3	US-08-789-333F-64	Sequence 64, Appli
C 42	9.2	61.3	18	4	US-08-787-738B-64	Sequence 64, Appli
C 43	9.2	61.3	20	1	US-08-212-252-6	Sequence 6, Appli
C 44	9.2	61.3	20	1	US-08-199-579-13	Sequence 13, Appli
C 45	9.2	61.3	20	1	US-08-263-413-5	Sequence 5, Appli

CURRENT FILING DATE: 2001-02-08
 NUMBER OF SEQ ID NOS: 154
 SEQ ID NO: 22
 LENGTH: 20

TYPE: DNA
 ORGANISM: Artificial Sequence

FEATURE:
 OTHER INFORMATION: Antisense Oligonucleotide

Query Match Best Local Similarity 72.0%; Score 10.8; DB 4; Length 20;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 GAUAACGUGAGAU 15
 Db 20 GCTGACGTGAGAT 7

RESULT 3
 US-08-182-968A-447/C
 Sequence 447, Application US/08182968A
 ; Patent No. 5610054
 GENERAL INFORMATION:
 APPLICANT: Draper, Kenneth G.
 TITLE OF INVENTION: METHOD AND REAGENT FOR
 INHIBITING HEPATITIS C
 TITLE OF INVENTION: VIRUS REPLICATION
 NUMBER OF SEQUENCES: 497

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/774,306A
 FILING DATE: December 26, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/182,968

FILING DATE: January 13, 1994

APPLICATION NUMBER: 07/882,888

FILING DATE: May 14, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 223/227

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 447:
 SEQUENCE CHARACTERISTICS:

LENGTH: 15

TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-774-306A-447
 Query Match Best Local Similarity 68.0%; Score 10.2; DB 2; Length 15;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAUACGUGAGAU 15
 Db 15 AGATAACGGCAGGT 1

SEQUENCE CHARACTERISTICS:
 LENGTH: 15
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

RESULT 5
 US-09-064-156A-447/C
 Sequence 447, Application US/09064156A
 ; Patent No. 6132966
 GENERAL INFORMATION:
 APPLICANT: Draper, Kenneth G.
 TITLE OF INVENTION: METHOD AND REAGENT FOR
 INHIBITING HEPATITIS C
 TITLE OF INVENTION: VIRUS REPLICATION
 NUMBER OF SEQUENCES: 498

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Los Angeles

US-08-182-968A-447
 Query Match Best Local Similarity 66.7%; Score 10.2; DB 1; Length 15;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAUACGUGAGAU 15
 Db 15 AGATAACGGCAGGT 1

STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/064,156A
 FILING DATE: April 21, 1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/774,306
 FILING DATE: December 26, 1996
 APPLICATION NUMBER: 08/182,968
 FILING DATE: January 13, 1994
 APPLICATION NUMBER: 07/882,888
 FILING DATE: May 14, 1992

ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 234/083

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510

SEQUENCE CHARACTERISTICS:
 LENGTH: 15
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SPORADENESS: single
 TOPOLOGY: linear

RESULT 6
 US-09-064-156A-447

Query Match 68.0%; Score 10.2; DB 3; Length 15;
 Best Local Similarity 66.7%; Pred. No. 3.8e+03;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAUAGCAGGAAAU 15
 ||||| ||| : ||||:
 Db 15 AGATACGACAAGGT 1

RESULT 7
 US-09-780-175-50/C

Sequence 50, Application US/09780175
 Patient No. 6440738

GENERAL INFORMATION:
 APPLICANT: Robert McKay
 APPLICANT: Susan M. Frasier
 APPLICANT: Jacqueline Wyatt
 TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-BETA EXPRESSION
 FILE REFERENCE: RUS-0164
 CURRENT APPLICATION NUMBER: US/09/780,175
 CURRENT FILING DATE: 2001-02-08
 NUMBER OF SEQ ID NOS: 154
 SEQ ID NO 50
 LENGTH: 20
 TYPE: DNA

FEATURE:
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Antisense Oligonucleotide

RESULT 8
 US-08-758-306-1325/C

Sequence 1325, Application US/08758306
 Patient No. 5807743

GENERAL INFORMATION:
 APPLICANT: Stinchcomb, Dan T.
 APPLICANT: McSwigan, James A.
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 TREATMENT OF DISEASES ASSOCIATED WITH
 TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
 TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
 NUMBER OF SEQUENCES: 1379

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories
 STREET: 100 Abbott Park Rd
 CITY: Abbott Park
 STATE: IL
 COUNTRY: USA
 ZIP: 60064

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street

STREET: Suite 4700
CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/758,306

FILING DATE: December 3, 1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 212/132

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1325:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-758-306-1325

RESULT 9

US-09-205-143-70/c

Sequence 70, Application US/09/205143

Patent No. 6,107,091

GENERAL INFORMATION:

APPLICANT: Lex M. Cowert

TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-16 EXPRESSION

FILE REFERENCE: RTS-032

CURRENT APPLICATION NUMBER: US/09/205,143

CURRENT FILING DATE: 1998-12-03

NUMBER OF SEQ ID NOS: 87

SEQ ID NO: 70

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-205-143-70

Query Match 65.3%; Score 9.8; DB 3; Length 18;

Best Local Similarity 76.9%; Pred. No. 6.5e+03; Mismatches 10; Conservatve 1; Indels 0; Gaps 0;

QY 1 AGAAUACGUGAG 13

DB 11 AGATTAAGGGGAG 1

RESULT 9

US-09-844-634-63

Sequence 63, Application US/09/844634

Patent No. 6,110,324

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Andrew T. Watt

TITLE OF INVENTION: ANTISENSE MODULATION OF TUMOR NECROSIS FACTOR RECEPTOR 2 EXPRESSION

FILE REFERENCE: RTS-0216

CURRENT APPLICATION NUMBER: US/09/844,634

CURRENT FILING DATE: 2001-04-27

NUMBER OF SEQ ID NOS: 174

SEQ ID NO: 63

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-844-634-63

Query Match 65.3%; Score 9.8; DB 4; Length 20;

Best Local Similarity 69.2%; Pred. No. 6.5e+03; Mismatches 9; Conservatve 2; Indels 0; Gaps 0;

QY 1 AGAAUACGUGAG 13

DB 2 AGCTAACTTGAG 14

RESULT 12

US-08-180-209B-5

Sequence 5, Application US/08/180209B

Patent No. 5,593,877

GENERAL INFORMATION:

APPLICANT: King, Te-Piao

TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND

TITLE OF INVENTION: HIALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED

TITLE OF INVENTION: THEREIN

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue

US-09-485-388-5

Query Match 64.0%; Score 9.6; DB 4; Length 17;
 Best Local Similarity 50.0%; Pred. No. 8.3e+03; Length 17;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAUACCGUGAGAU 15
 Db 1 GAYACNGTNAARAT 14

RESULT 15

US-08-474-853-5

Sequence 5, Application US/08474853

Patent No. 6287559

GENERAL INFORMATION:

APPLICANT: King, Te-Piao

TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF

TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND

TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/474,853

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/180,209

FILING DATE: 11-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/031,400

FILING DATE: 11-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-074 CIRP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-474-853-5

Query Match 64.0%; Score 9.6; DB 4; Length 17;
 Best Local Similarity 50.0%; Pred. No. 8.3e+03; Length 17;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAUACCGUGAGAU 15
 Db 1 GAYACNGTNAARAT 14

Search completed: May 22, 2003, 20:18:23
 Job time : 35.277 secs

GenCore version 5.1.4_p5_4578
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Om nucleic - nucleic search, using sw model

Run on: May 22, 2003, 19:36:48 ; Search time 70.9091 Seconds
(without alignments)
27.9.329 Million cell updates/sec

Title: US-09-780-929-97
Perfect score: 15
Sequence: 1 agauaacgugaagau 15

Scoring table: IDENTITY_NDIC Gapext 1.0

Searched: 828747 seqs. 660231138 residues

Total number of hits satisfying chosen parameters: 191488

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA.*

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2: /cgn2_6/ptodata/1/pubpna/PET_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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6: /cgn2_6/ptodata/1/pubpna/PUBCOMB.seq:*
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9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

RESULT 1
US-09-780-929-97
Sequence 97, Application US/09780929
Patient No. US20020151693AI
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc
APPLICANT: Breaker, Ronald
APPLICANT: Beigelman, Leo
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
FILE REFERENCE: MBIB00-884-H (500/001)
CURRENT APPLICATION NUMBER: US/09-780-929
CURRENT FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: US 60/181,360
PRIOR FILING DATE: 2000-02-08
SOFTWARE: Patentin version 3.0
NUMBER OF SEQ ID NOS: 126
SEQ ID NO 97
LENGTH: 15
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Description of Artificial Sequence:
US-09-780-929-97
Query Match 100.0%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAUAAACGGAGAGAU 15

RESULT 2
US-09-730-289B-605/c
Sequence 605, Application US/09730289B
Publication No. US20030050259AI
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease

ALIGNMENTS

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	15	10	US-09-780-929-97 Sequence 97, Appl
C 2	10.8	72.0	17	9	US-09-730-289B-606 Sequence 606, Appl
C 3	10.8	72.0	17	9	US-09-730-289B-607 Sequence 607, Appl
C 4	10.8	72.0	18	9	US-09-213-329-4 Sequence 4, Appl
C 5	10.4	69.3	19	10	US-09-969-373-2697 Sequence 2697, Appl
C 6	10.2	68.0	15	10	US-09-504-231A-469 Sequence 469, Appl
C 7	10.2	68.0	15	10	US-09-274-553D-469 Sequence 469, Appl
C 8	10.2	68.0	19	9	US-10-000-773A-6 Sequence 6, Appl
C 9	9.8	65.3	17	9	US-09-776-474-739 Sequence 739, Appl
C 10	9.8	65.3	17	9	US-09-776-474-739 Sequence 959, Appl
C 11	9.8	65.3	20	9	US-09-918-187-64 Sequence 64, Appl
C 12	9.8	65.3	20	10	US-09-880-631-141 Sequence 141, Appl
C 13	9.4	62.7	17	9	US-09-730-289B-596 Sequence 596, Appl
C 14	9.4	62.7	18	10	US-09-878-582-29 Sequence 29, Appl
C 15	9.4	62.7	18	10	US-09-959-373-4497 Sequence 4497, Appl
C 16	9.4	62.7	19	10	US-09-959-373-4497 Sequence 1862, Appl
C 17	9.4	62.7	20	9	US-09-917-963-42 Sequence 42, Appl
C 18	9.4	62.7	20	9	US-09-955-611-56 Sequence 56, Appl
C 19	9.4	62.7	20	10	US-09-752-983-112 Sequence 112, Appl

FILE REFERENCE: MBH00-864-A (400/006)
; CURRENT APPLICATION NUMBER: US/09/730,289B
; CURRENT FILING DATE: 2000-12-05
; PRIORITY APPLICATION NUMBER: US 60/169,100
; PRIORITY FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 3897
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 606
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-730-289B-606

Qy	1 AGAUUACGUGAGA 14	Db	17 AGATAACATGAGGA 4
Query Match	72.0%; Score 10.8; DB 9; Length 17;		
Best Local Similarity	71.4%; Pred. No. 1.3e+04; 2; Mismatches		
Matches	10; Conservative 2; Indels 0; Gaps 0;		

RESULT 3
US-09-730-289B-607/c
; Sequence 607, Application US/09730289B
; Publication No. US20030050259A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Harry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
; FILE REFERENCE: MBHB00-864-A (400/006)
; CURRENT APPLICATION NUMBER: US/09/730,289B
; CURRENT FILING DATE: 2000-12-05
; PRIORITY APPLICATION NUMBER: US 60/169,100
; PRIORITY FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 3897
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 607
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-730-289B-607

Qy	1 AGAUUACGUGAGA 14	Db	17 AGATAACATGAGGA 4
Query Match	72.0%; Score 10.8; DB 9; Length 17;		
Best Local Similarity	71.4%; Pred. No. 1.3e+04; 2; Mismatches		
Matches	10; Conservative 2; Indels 0; Gaps 0;		

RESULT 4
US 10-213-329-4
; Sequence 4, Application US/10213329
; Publication No. US20030083465A1
; GENERAL INFORMATION:
; APPLICANT: Zimrin, Ann B.
; APPLICANT: MacIag, Thomas
; APPLICANT: Wong, Michael K.K.
; APPLICANT: Pepper, Michael S.
; APPLICANT: Montesano, Roberto
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND COMPOSITIONS
; TITLE OF INVENTION: BASED ON JAGGED/NOTCH PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: 0036-1U1
; CURRENT FILING DATE: 2002-08-06
; PRIORITY APPLICATION NUMBER: US/09/199,865
; PRIORITY FILING DATE: 1998-11-25
; PRIORITY APPLICATION NUMBER: 60/018,841
; PRIORITY FILING DATE: 1996-05-31
; PRIORITY APPLICATION NUMBER: PCT/US97/09407

Qy	1 AGAUUACGUGAGA 14	Db	15 AGATAATGAGGAA 2
Query Match	72.0%; Score 10.8; DB 9; Length 17;		
Best Local Similarity	71.4%; Pred. No. 1.3e+04; 2; Mismatches		
Matches	10; Conservative 2; Indels 0; Gaps 0;		

RESULT 5
US-09-969-373-2697/c
; Sequence 2697, Application US/09969373
; Patent No. US2002013852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Haage, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(2679)A
; CURRENT APPLICATION NUMBER: US/09/969, 373
; CURRENT FILING DATE: 2001-10-02
; PRIORITY APPLICATION NUMBER: US 09/754, 853
; PRIORITY FILING DATE: 2001-01-05
; PRIORITY APPLICATION NUMBER: US 09/760,427
; PRIORITY FILING DATE: 2001-01-13
; PRIORITY APPLICATION NUMBER: US 09/655, 768
; PRIORITY FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 2697
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Glycine max
; US-09-969-373-2697

Qy	1 AGAUUACGUGAGA 12	Db	17 AGACAACGTGAA 6
Query Match	69.3%; Score 10.4; DB 10; Length 19;		
Best Local Similarity	68.3%; Pred. No. 2.1e+04; 1; Mismatches		
Matches	10; Conservative 1; Indels 0; Gaps 0;		

RESULT 6
US-09-504-231A-69/c
; Sequence 469, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Maciejak, Dennis
; TITLE OF INVENTION: ENZYMMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATED TO INFECTION
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIORITY APPLICATION NUMBER: 09/274,553
; PRIORITY FILING DATE: 1999-03-23
; PRIORITY APPLICATION NUMBER: 09/257,608
; PRIORITY FILING DATE: 1999-02-24

PRIOR APPLICATION NUMBER: 60/100, 842
 PRIOR FILING DATE: 1998-09-18
 PRIORITY NUMBER: 60/083, 217
 PRIOR FILING DATE: 1998-04-27
 NUMBER OF SEQ ID NOS: 3242
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 469
 LENGTH: 15
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
 Query Match 68.0%; Score 10.2; DB 10; Length 15;
 Best Local Similarity 66.7%; Pred. No. 2.7e+04;
 Matches 10; Conservative 2; Mismatches 3;
 Indels 0; Gaps 0;
 QY 1 AGAUACGUGAGAU 15
 |||:||| |||:
 Db 15 AGATACGACAGGT 1
 RESULT 7
 US-09-274-553D-469/c
 Sequence 469, Application US/09274553D
 Patent No. US2002008225A1
 GENERAL INFORMATION:
 APPLICANT: Blatt, Lawrence
 APPLICANT: McSwiggen, James
 APPLICANT: Roberts, Beth
 APPLICANT: Pavco, Pamela
 APPLICANT: Maciejak, Dennis
 TITLE OF INVENTION: ENZYMIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATED TO HEPATITIS C VIRUS INFECTION
 FILE REFERENCE: PPI 247/282
 CURRENT APPLICATION NUMBER: US/09/274, 553D
 CURRENT FILING DATE: 1999-03-23
 PRIOR APPLICATION NUMBER: 09/257, 608
 PRIOR FILING DATE: 1999-02-24
 PRIOR APPLICATION NUMBER: 60/100, 842
 PRIOR FILING DATE: 1998-09-18
 PRIOR FILING DATE: 1998-04-27
 NUMBER OF SEQ ID NOS: 3148
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 469
 LENGTH: 15
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
 Query Match 68.0%; Score 10.2; DB 10; Length 15;
 Best Local Similarity 66.7%; Pred. No. 2.7e+04;
 Matches 10; Conservative 2; Mismatches 3;
 Indels 0; Gaps 0;
 QY 1 AGAUACGUGAGAU 15
 |||:||| |||:
 Db 15 AGATACGACAGGT 1
 RESULT 8
 US-10-000-773A-6
 Sequence 6, Application US/10000773A
 Publication No. US20030069195A1
 GENERAL INFORMATION:
 APPLICANT: Farrar, Gwenyth Jane
 APPLICANT: Humphries, Peter
 APPLICANT: Kenna, Paul
 APPLICANT: Millington-Ward, Sophia
 TITLE OF INVENTION: Suppression of Polymorphic Alleles
 RESULT 9
 US-09-776-474-739
 Sequence 739, Application US/09776474
 Publication No. US20030087847A1
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Jarvis, Thale
 APPLICANT: Boher, Robert
 APPLICANT: Holman, Patricia
 APPLICANT: Fattaey, Ali
 APPLICANT: McSwiggen, Jim
 TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CK1) by Enzyme Inhibition
 FILE REFERENCE: MBHR00-955-A (400/008)
 CURRENT APPLICATION NUMBER: US/09/776, 474
 PRIOR APPLICATION NUMBER: 05/09/776, 474
 CURRENT FILING DATE: 2001-05-02
 PRIOR FILING DATE: 2000-03-02
 NUMBER OF SEQ ID NOS: 2992
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 739
 LENGTH: 17
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
 Query Match 65.3%; Score 9.8; DB 9; Length 17;
 Best Local Similarity 84.6%; Pred. No. 4.4e+04;
 Matches 11; Conservative 0; Mismatches 2;
 Indels 0; Gaps 0;
 QY 1 AGAUACGUGAG 13
 |||:||| |||:
 Db 2 AGAAAUGUGAAG 14
 RESULT 10
 US-09-776-474-959
 Sequence 959, Application US/09776474
 Publication No. US20030087847A1
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Jarvis, Thale
 APPLICANT: Boher, Robert

APPLICANT: Holman, Patricia
 APPLICANT: Fattney, Ali
 APPLICANT: McSwiggen, Jim
 TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK1)
 FILE REFERENCE: MHB00-955-A (400/008)
 CURRENT APPLICATION NUMBER: US/09/776,474
 CURRENT FILING DATE: 2001-02-02
 PRIOR APPLICATION NUMBER: US 60/179,983
 NUMBER OF SEQ ID NOS: 2992
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 959
 LENGTH: 17
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
 ; US-09-776,474-959
 Query Match 65.3%; Score 9.8; DB 9; Length 17;
 Best Local Similarity 84.6%; Pred. No. 4 4e+04;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 AGAAUACGUGAG 13
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 Db 4 AGAAAUGUGAG 16
 RESULT 11
 US-09-918-187-64
 Sequence 64, Application US/09918187
 Publication No. US20030083282A1
 GENERAL INFORMATION:
 APPLICANT: Rosanne M. Crooke
 APPLICANT: Mark J. Graham
 TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
 FILE REFERENCE: ISPH-0590
 CURRENT APPLICATION NUMBER: US/09/918,187
 CURRENT FILING DATE: 2001-07-30
 NUMBER OF SEQ ID NOS: 80
 SEQ ID NO 64
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: Antisense Oligonucleotide
 ; US-09-918-187-64
 Query Match 65.3%; Score 9.8; DB 9; Length 20;
 Best Local Similarity 61.5%; Pred. No. 4 5e+04;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 ABRACGUGAAGAU 15
 ||||| ;|||||
 Db 4 ATATCCCTGAGAT 16
 RESULT 12
 US-09-800-631-141C
 Sequence 141, Application US/09800631
 Patent No. US2002009228A1
 GENERAL INFORMATION:
 APPLICANT: Hong Zhang
 APPLICANT: Jacqueline Wyatt
 TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST EXPRESSION
 FILE REFERENCE: ISPH-0544
 CURRENT APPLICATION NUMBER: US/09/800,631
 CURRENT FILING DATE: 2001-03-07
 PRIOR APPLICATION NUMBER: US/09/657,346
 PRIOR FILING DATE: 2000-09-07
 NUMBER OF SEQ ID NOS: 175
 SEQ ID NO 141
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Antisense Oligonucleotide
 ; US-09-800-631-141
 Query Match 65.3%; Score 9.8; DB 10; Length 20;
 Best Local Similarity 69.2%; Pred. No. 4.5e+04;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 AGAACACGGAG 13
 ||||| :|||
 Db 13 AGATACATGTAG 1
 RESULT 13
 US-09-730-2899-596
 Sequence 596, Application US/09730289B
 Publication No. US20030050259A1
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Blatt, Larry
 APPLICANT: McSwiggen, Jim
 TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
 FILE REFERENCE: MHB00-864-A (400/006)
 CURRENT APPLICATION NUMBER: US/09/730,289B
 CURRENT FILING DATE: 2000-12-05
 PRIOR APPLICATION NUMBER: US 60/169,100
 PRIOR FILING DATE: 1999-12-06
 NUMBER OF SEQ ID NOS: 3897
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 596
 LENGTH: 17
 TYPE: RNA
 ORGANISM: Homo sapiens
 ; US-09-730-289B-596
 Query Match 62.7%; Score 9.4; DB 9; Length 17;
 Best Local Similarity 90.9%; Pred. No. 7.3e+04;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 AUACCGUGAG 13
 ||||| |||||
 Db 4 AUUACAUAGAA 14
 RESULT 14
 US-09-878-582-29/C
 Sequence 29, Application US/09878582
 Patent No. US20020058638A1
 GENERAL INFORMATION:
 APPLICANT: Brett P. Monia
 APPLICANT: Lex M. Cowert
 APPLICANT: Robert McKay
 TITLE OF INVENTION: ANTISENSE MODULATION OF PTEN EXPRESSION
 FILE REFERENCE: ISPH-0463
 CURRENT APPLICATION NUMBER: US/09/878,582
 CURRENT FILING DATE: 2001-06-11
 PRIOR APPLICATION NUMBER: 09/577,902
 PRIOR FILING DATE: 2000-05-24
 PRIOR APPLICATION NUMBER: US 09/358,381
 PRIOR FILING DATE: 1999-07-21
 PRIOR APPLICATION NUMBER: PCT/US99/29594
 PRIOR FILING DATE: 1999-12-14
 NUMBER OF SEQ ID NOS: 51
 SEQ ID NO 29
 LENGTH: 18
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Antisense Oligonucleotide
 ; US-09-878-582-29

Query Match 62.7%; Score 9.4; DB 10; Length 18;
 Best Local Similarity 72.7%; Pred. No. 7, 3e+04;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AACGUGAGAU 15
 Db 17 AAGGTGAGAT 7

RESULT 15

; Sequence 4497, Application US/09969373

Patent No. US20020133852A1

GENERAL INFORMATION:

APPLICANT: Effertz, Roger J.

APPLICANT: Hauge, Brian M.

TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping

FILE REFERENCE: 38-10(55679)A

CURRENT APPLICATION NUMBER: US/09/969,373

CURRENT FILING DATE: 2001-10-02

PRIOR APPLICATION NUMBER: US 09/754,853

PRIOR FILING DATE: 2001-01-05

PRIOR APPLICATION NUMBER: US 09/760,427

PRIOR FILING DATE: 2001-01-13

PRIOR APPLICATION NUMBER: US 09/555,768

PRIOR FILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 4593

SEQ ID NO 4497

LENGTH: 18

TYPE: DNA

ORGANISM: Glycine max

US-09-569-373-4497

Query Match 62.7%; Score 9.4; DB 10; Length 18;
 Best Local Similarity 72.7%; Pred. No. 7, 3e+04;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GAUAAACGUGAU 12
 Db 13 GATAAACGTTGCA 3

Search completed: May 22, 2003, 21:38:46
 Job time : 72.9091 secs

Run on: May 22, 2003, 18:59:38 ; Search time 1728.64 Seconds
 (without alignments)
 218,170 Million cell updates/sec

OM nucleic - nucleic search, using sw model

Title: US-09-780-929-97

Perfect score: 15

Sequence: 1 agauaaacggagaa 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 1600790

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Pending:

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 49: /cgn2_-6/ptodata/1/pna/us6005_COMB.seq: *
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 51: /cgn2_-6/ptodata/1/pna/us6007_COMB.seq: *
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 63: /cgn2_-6/ptodata/1/pna/us6019_COMB.seq: *
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44: Sequence 50, Appl
 Sequence 13493, A
 Sequence 607, App
 Sequence 4, Appl
 Sequence 12, Appl
 Sequence 4, Appl
 Sequence 5954, Ap
 Sequence 27, Appl
 Sequence 50, Appl
 Sequence 12603, A
 Sequence 15028, A
 Sequence 12172, A
 Sequence 12172, A
 Sequence 12172, A
 Sequence 217, App
 Sequence 217, App

The Pending database search results should not be left in the case because they contain data that is confidential.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, .rnlpn and .rnppn

Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets of results, with the extensions, .rnppn and .rnpm

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions, .rapm and .rapn

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, .rnpm and .rnppn

The Pending database search results should not be left in the case because they contain data that is confidential.

RESULT 13
PCT-US02-03159-22/c
; Sequence 22, Application PCTUS0203159
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Robert McKay
; APPLICANT: Susan M. Freier
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-BETA EXPRESSION
; FILE REFERENCE: RTSP-0270
; CURRENT APPLICATION NUMBER: PCT/US02/03159
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US02-03159-22

Query Match 72.0%; Score 10.8; DB 65; Length 18;
Best Local Similarity 64.3%; Pred. No. 1e+05; 2; Indels 0; Gaps 0;
Matches 9; Conservative 3; Mismatches 3

Qy 2 GAUAACGUGAGAU 15
Db 2 GATRACGGGCAAT 15

RESULT 14
US-09-068-506-50/c
; Sequence 50, Application US/09068506A
; GENERAL INFORMATION:
; APPLICANT: YASUE, Hirofumi
; APPLICANT: YOSHIMURA, Kumamoto
; TITLE OF INVENTION: DIAGNOSIS OF DISEASES ASSOCIATED WITH CORONARY
; FILE REFERENCE: 0032-245P
; CURRENT APPLICATION NUMBER: US/09/068,506A
; CURRENT FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primers
US-09-068-506-50

Query Match 72.0%; Score 10.8; DB 14; Length 20;
Best Local Similarity 64.3%; Pred. No. 1e+05; 2; Indels 0; Gaps 0;
Matches 9; Conservative 3; Mismatches 2

Qy 2 GAUAACGUGAGAU 15
Db 20 GGTGACCTGAGAT 7

Search completed: MAY 22, 2003, 21:22:03
Job time : 1731.64 secs

GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)B
; CURRENT APPLICATION NUMBER: US/09/554,000
; CURRENT FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 15034
; SEQ ID NO 12603
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-09-514-000-12603

Query Match 72.0%; Score 10.8; DB 19; Length 20;
Best Local Similarity 64.3%; Pred. No. 1e+05; 2; Indels 0; Gaps 0;
Matches 9; Conservative 3; Mismatches 2

Qy 2 GAUAACGUGAGAU 15
Db 20 GATGACCTGAGAT 7

Gencore version 5.1.4_P5_458
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Om nucleic - nucleic search, using sw model

Run on:

May 22, 2003, 19:04:38 ; search time 371.364 seconds

(without alignments)

209.509 Million cell updates/sec

Title: US-09-780-929-97

Perfect score: 15

Sequence: 1 agauaacgugaagau 15

Scoring table: IDENTITY_NUC

Scoring table: Gapop 10.0 , Gapext 1.0

Searched: 6438716 seqs, 2593467500 residues

Total number of hits satisfying chosen parameters: 667140

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
c 1	11.8	78.7	20	9	US-10-316-389-88
c 2	11.4	76.0	20	1	PCT-US02-38622-50
c 3	11	73.3	15	9	US-10-287-819-374
c 4	11	73.3	15	9	US-10-287-818-836
c 5	10.8	72.0	19	9	US-10-310-188-47798
c 6	10.8	72.0	20	9	US-10-302-027-46
c 7	10.8	72.0	20	9	US-10-302-027-106
c 8	10.4	69.3	16	8	US-10-331-109-21
c 9	10.4	69.3	17	6	US-10-846-903-24
c 10	10.4	69.3	17	9	US-10-310-188-80491
c 11	10.4	69.3	19	1	PCT-US03-03662-97
c 12	10.4	69.3	19	1	PCT-US03-03662-336
c 13	10.4	69.3	19	9	US-10-310-188-14089
c 14	10.4	69.3	20	1	PCT-US02-38805-82
c 15	10.4	69.3	20	8	US-10-317-277R-73
c 16	10.4	69.3	20	8	US-10-317-277A-148
c 17	10.2	68.0	15	6	US-10-274-553E-469
c 18	10.2	68.0	17	9	US-10-310-188-22900
c 19	10.2	68.0	19	1	PCT-US02-34679-118
c 20	10.2	68.0	19	9	US-10-282-174-118
c 21	10.2	68.0	19	9	US-10-293-338-4500
c 22	10.2	68.0	19	9	US-10-349-143-1465

RESULT 1
US-10-316-389-88/C

; Sequence 88, Application US/10316389

GENERAL INFORMATION:

APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: ANTISENSE MODULATION OF ABCC2 EXPRESSION

FILE REFERENCE: RUS-0382

CURRENT APPLICATION NUMBER: US/10/316,389

CURRENT FILING DATE: 2002-12-10

NUMBER OF SEQ ID NOS: 143

SEQ ID NO 88

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE: OTHER INFORMATION: Antisense oligonucleotide

US-10-316-389-88

Query Match 78.7%; Score 11.8; DB 9; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.e+04; 1; Mismatches 2; Indels 0; Gaps 0;

Matches 12; Conservative 1; Sequence 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGUAACCGUGAAGAU 15
||| ||| |||||:
Db 15 AGCAACGGAAAGAT 1

RESULT 2

PCT-US02-38622-50/C

; Sequence 50, Application PC/RUS0238622

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Susan M. Frasier

APPLICANT: Isis Pharmaceuticals, Inc.

TITLE OF INVENTION: ANTISENSE MODULATION OF SHIP-1 EXPRESSION

FILE REFERENCE: RUS-0447

CURRENT APPLICATION NUMBER: PCT/US02/38622

CURRENT FILING DATE: 2002-12-04

PRIOR APPLICATION NUMBER: 10/003,919

PRIOR FILING DATE: 2001-12-06

NUMBER OF SEQ ID NOS: 87

SEQ ID NO 50

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

Sequence 110, App
Sequence 212, App
Sequence 35003, A
Sequence 86, App
Sequence 161, App
Sequence 2145, App
Sequence 2146, App
Sequence 3267, App
Sequence 3268, App
Sequence 32654, A
Sequence 1129, App
Sequence 4481, App
Sequence 5747, App
Sequence 1129, App
Sequence 2145, App
Sequence 2146, App
Sequence 3267, App
Sequence 3268, App
Sequence 1165, App
Sequence 94, Appl
Sequence 94, Appl
Sequence 723, App
Sequence 1246, App

Sequence 110, App
Sequence 212, App
Sequence 35003, A
Sequence 86, App
Sequence 161, App
Sequence 2145, App
Sequence 2146, App
Sequence 3267, App
Sequence 3268, App
Sequence 32654, A
Sequence 1129, App
Sequence 4481, App
Sequence 5747, App
Sequence 1129, App
Sequence 2145, App
Sequence 2146, App
Sequence 3267, App
Sequence 3268, App
Sequence 1165, App
Sequence 94, Appl
Sequence 94, Appl
Sequence 723, App
Sequence 1246, App

FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; PCT-US02-38622-50

Query Match 76.0%; Score 11.4; DB 1; Length 20;
 Best Local Similarity 84.6%; Pred. No. 1.8e+04; Indels 0; Gaps 0;
 Matches 11; Conservative 1; Mismatches 1;

QY 2 GUAACGGUGAGAU 14
 Db 20 GACAACGTGAGA 8

SOFTWARE: Proprietary
 SEQ ID NO 374
 LENGTH: 15
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-287-818-374

; Sequence 374, Application US/10287818
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Vibrio cholerae chromosome I, complete chromosome.
; FILE REFERENCE: Jim Zeegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,818
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 1318
; SOFTWARE: Proprietary
; SEQ ID NO 374
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Vibrio cholerae chromosome I, complete chromosome.
; FEATURE:
; LOCATION: (810101)..(810115)
; OTHER INFORMATION: Chromosome - 1 Strand = positive ConnectronObjectNumber = 534

Query Match 73.3%; Score 11; DB 9; Length 15;
 Best Local Similarity 81.8%; Pred. No. 2.9e+04; Indels 0; Gaps 0;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 AACGUGAGAU 15
 Db 1 AACGTGAGAT 11

RESULT 4
 US-10-287-818-836

; Sequence 836, Application US/10287818
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Vibrio cholerae chromosome I, complete chromosome.
; FILE REFERENCE: Jim Zeegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,818
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 1318
; SOFTWARE: Proprietary
; SEQ ID NO 836
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Vibrio cholerae chromosome I, complete chromosome.

RESULT 5
 US-10-310-188-47798

; Sequence 188, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G PROTEINS
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 47798
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-310-188-47798

RESULT 6
 US-10-302-027-46/c

; Sequence 46, Application US/10302027
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF GANKYRIN EXPRESSION
; FILE REFERENCE: PTS-0068
; CURRENT APPLICATION NUMBER: US/10/302,027
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 46
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-10-302-027-46

Query Match 72.0%; Score 10.8; DB 9; Length 19;
 Best Local Similarity 71.4%; Pred. No. 3.8e+04; Indels 0; Gaps 0;
 Matches 10; Conservative 2; Mismatches 2;

QY 2 GUAACGGUGAGAU 15
 Db 2 GAGACATGAGAT 15

RESULT 7
 US-10-302-027-106

; Sequence 106, Application US/10302027
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF GANKYRIN EXPRESSION
; FILE REFERENCE: PTS-0068
; CURRENT APPLICATION NUMBER: US/10/302,027
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 106
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; US-10-302-027-106

Query Match 72.0%; Score 10.8; DB 9; Length 20;
 Best Local Similarity 64.3%; Pred. No. 3.8e+04;

RESULT 5
 US-10-310-188-47798

Matches: 9; Conservative: 3; Mismatches: 2; Indels: 0; Gaps: 0; Db: 16 GACAACGTGAAG 5

Qy 2 GAUACCGUGAGAU 15
| :||| :||||: 7 GGTAACGTGAAAGAT 20

RESULT 8
US-10-331-109-21/C
Sequence 21, Application US/10331109
GENERAL INFORMATION:
APPLICANT: BICKEL, et al.
TITLE OF INVENTION: Method for the qualitative and/or quantitative detection of maled
TITLE OF INVENTION: interactions on probe arrays
FILE REFERENCE: 12671/1
CURRENT APPLICATION NUMBER: US/10/331.109
CURRENT FILING DATE: 2002-12-27
PRIORITY APPLICATION NUMBER: PCT/EP01/07575
PRIORITY FILING DATE: 2001-07-02
PRIORITY APPLICATION NUMBER: DE 100 33 334.6
PRIORITY FILING DATE: 2000-07-01
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Description of the artificial sequence:
US-10-331-109-21

Query Match 69.3%; Score 10.4; DB 8; Length 16;
Best Local Similarity 66.7%; Pred. No. 6.2e+04; Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 UUACGGUGAGAU 15
| :|||:||||: 13 TAAAGGAGAT 2

Db 13 ATAACGTGAAAGAT 2

RESULT 9
US-09-846-903-24/C
Sequence 24, Application US/09846903
GENERAL INFORMATION:
APPLICANT: Conner, Timothy W.
APPLICANT: Dubois, Patrice
APPLICANT: Malven, Marianne
APPLICANT: Masucci, James D.
TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL
TITLE OF INVENTION: OF GENE EXPRESSION
FILE REFERENCE: 38-21(15678)B Promoters
CURRENT APPLICATION NUMBER: US/09/846,903
CURRENT FILING DATE: 2001-04-26
PRIORITY APPLICATION NUMBER: US 60/201,255
PRIORITY FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
LENGTH: 17
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: fully
US-09-846-903-24

Query Match 69.3%; Score 10.4; DB 6; Length 17;
Best Local Similarity 83.3%; Pred. No. 6.2e+04; Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GAUACCGUGAG 13
| :|||:||||: 11

RESULT 10
US-10-310-188-80491/C
Sequence 80491, Application US/10310188
GENERAL INFORMATION:
APPLICANT: RosettaGenomics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 80491
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-10-310-188-80491
Query Match 69.3%; Score 10.4; DB 9; Length 17;
Best Local Similarity 75.0%; Pred. No. 6.2e+04; Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AUUACCGUGAGA 14
| :|||:||||: 15 ATAACGTGAAA 4

Db 15 ATAACGTGAAA 4

RESULT 11
PCT-US03-03662-97/C
Sequence 97, Application PC/TUS0303662
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
APPLICANT: Thomson, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Cyclin D1 Gene Express
FILE REFERENCE: 02-11005-A (400/083)
CURRENT APPLICATION NUMBER: PCT/US03/03662
CURRENT FILING DATE: 2003-02-06
PRIORITY APPLICATION NUMBER: US 60/411,275
PRIORITY FILING DATE: 2002-09-17
PRIORITY APPLICATION NUMBER: US 60/358,580
PRIORITY FILING DATE: 2002-02-20
PRIORITY APPLICATION NUMBER: US 60/363,124
PRIORITY FILING DATE: 2002-03-11
PRIORITY APPLICATION NUMBER: US 60/386,782
PRIORITY FILING DATE: 2002-06-06
PRIORITY APPLICATION NUMBER: US 60/406,784
PRIORITY FILING DATE: 2002-08-29
PRIORITY APPLICATION NUMBER: US 60/408,378
PRIORITY FILING DATE: 2002-09-05
PRIORITY APPLICATION NUMBER: US 60/409,293
PRIORITY FILING DATE: 2002-09-09
PRIORITY APPLICATION NUMBER: US 60/440,129
PRIORITY FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 530
SOFTWARE: Patentin version 3.2
SEQ ID NO 97
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/sINA sens
PCT-US03-03662-97
Query Match 69.3%; Score 10.4; DB 1; Length 19;
Best Local Similarity 75.0%; Pred. No. 6.2e+04; Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AUAACGUGAAGA 14
 |:||| ||:|||
 Db 12 ATAACTGTGAGA 1

RESULT 12
; PCT-US03-03662-336
; Sequence 336, Application PC/TUS0303662
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Cyclin D1 Gene Expression
; FILE REFERENCE: 02-1005-A (400/983)
; CURRENT APPLICATION NUMBER: PCT-US03/03662
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/411,275
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 336
; LENGTH: 19
; TYPE: RNA
; FEATURE:
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: sINA antisense region
; PCT-US03-03662-336

Query Match 69.3%; Score 10.4; DB 1; Length 19;
; Best Local Similarity 91.7%; Pred. No. 6.2e+04; Mismatches 0; Indels 0; Gaps 0;
; Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AUAACGUGAAGA 14
 |:||| ||:|||
 Db 8 AUAGGUGAAGA 19

RESULT 13.
; US-10-310-188-14089
; Sequence 14089, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGemomics
; TITLE OF INVENTION: BIOTINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 14089
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-310-188-14089

Query Match 69.3%; Score 10.4; DB 9; Length 19;
; Best Local Similarity 83.3%; Pred. No. 6.2e+04;
; Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AUAACGUGAAGA 14
 |:||| :|||
 Db 20 ATAACCTGGAGA 9

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
; Qy 2 GUAACGUGAAG 13
; |:||| |||
; Db 8 GATACACGGGAG 19

RESULT 14
; PCT-US02-38806-82
; Sequence 82, Application PC/TUS0238806
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; APPLICANT: Therianos, Stavros
; APPLICANT: Zhu, Min
; APPLICANT: Coleman, Paul
; TITLE OF INVENTION: MULTIPLEX REAL-TIME QUANTITATIVE PCR
; FILE REFERENCE: 21108 0009P1
; CURRENT APPLICATION NUMBER: PCT-US02/38806
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/397,475
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/336,095
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
; PCT-US02-38806-82

Query Match 69.3%; Score 10.4; DB 1; Length 20;
; Best Local Similarity 83.3%; Pred. No. 6.2e+04; Mismatches 1; Indels 0; Gaps 0;
; Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AUAACGUGAAGA 14
 |:||| :|||
 Db 8 ACAAGCTGAGA 19

RESULT 15
; US-10-317-277A-73/c
; Sequence 73, Application US/10317277A
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; TITLE OF INVENTION: Modulation of Estrogen-Responsive Finger Protein Expression
; FILE REFERENCE: RIS-043
; CURRENT APPLICATION NUMBER: US/10/317,277A
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial
; OTHER INFORMATION: Antisense Oligonucleotide
; US-10-317-277A-73

Query Match 69.3%; Score 10.4; DB 8; Length 20;
; Best Local Similarity 75.0%; Pred. No. 6.2e+04; Mismatches 1; Indels 0; Gaps 0;
; Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AUAACGUGAAGA 14
 |:||| :|||
 Db 20 ATAACCTGGAGA 9

Search completed: May 22, 2003, 21:35:56
Job time : 374.364 secs

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score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model

Run on:

May 22, 2003, 16:53:27 ; Search time 1045.64 Seconds

(without alignments)

500.987 Million cell updates/sec

Title: US-09-780-929-98
 Perfect score: 18
 Sequence: 1 aauggcctaucggugcga 18

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched:

2054610 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters:

332216

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: GenEmbl:*

2: gb_ba:*

3: gb_btg:*

4: gb_in:*

5: gb_om:*

6: gb_ov:*

7: gb_pat:*

8: gb_ph:*

9: gb_pl:*

10: gb_pr:*

11: gb_rps:*

12: gb_sf:*

13: gb_uni:*

14: gb_vir:*

15: em_ba:*

16: em_futn:*

17: em_hum:*

18: em_in1:*

19: em_mui:*

20: em_on1:*

21: em_or1:*

22: em_ovr:*

23: em_pat:*

24: em_phi:*

25: em_p1:*

26: em_r0:*

27: em_sts:*

28: em_uni:*

29: em_v1:*

30: em_hrg_hum:*

31: em_hrg_inv:*

32: em_hrg_other:*

33: em_hrg_mus:*

34: em_hrg_p1n:*

35: em_hrg_r0d:*

36: em_hrg_man:*

37: em_hrg_vrt:*

38: em_sy:*

39: em_hrgo_hum:*

40: em_hrgo_mus:*

41: em_hrgo_other:*

RESULT 1
 AX214296
 DEFINITION Sequence 109 from Patent WO0159102.
 ACCESSION AX214296
 VERSION AX214296.1 GI:15524373
 KEYWORDS SOURCE synthetic construct.
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Breaker, R. and Emilsson, G.
 TITLE Nuclezymes with endonuclease activity
 Patent: WO 0159102-A 109 16-AUG-2001;
 RIPOZYME PHARMACEUTICALS, INC. (US); Yale University (US)

Pred. No. is the number of results predicted by chance to have a

	FH FT	KEY source	Location/Qualifiers				
FEATURES		Location/Qualifiers	1. . .20 /organism="Unidentified".				
source			1. . .20 /db_xref="taxon:32044" /organism="unidentified"				
BASE COUNT		7 a	7 c	4 g	2 t		
ORIGIN							
QY	4	GGCCUAUCGGUGC 16					
Db	2	GGCCCTGCGGNGC 14					
RESULT 8							
AR115440		AR115440					
LOCUS		Sequence 1886 from patent US 6132967.					
DEFINITION			17 bp DNA				
ACCESSION			PAT 16-MAY-2001				
VERSION							
KEYWORDS							
SOURCE							
ORGANISM		Unknown.					
REFERENCE		Unclassified.					
AUTHORS		1 (bases 1 to 17)					
JOURNAL		Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.					
FEATURES		Best Local Similarity 69.2%; Pred. No. 1.5e+05; Matches 9; Conservative 1; Indels 0; Gaps 0;					
source		1. . .17 /organism="unknown"					
BASE COUNT		1 a	5 c	7 g	4 t		
ORIGIN							
QY	4	GGCCUAUCGGUGC 16					
Db	2	GGCCCTGCGGNGC 14					
RESULT 9							
AR115531		AR115531					
LOCUS		Sequence 1977 from patent US 6132967.					
DEFINITION		17 bp DNA					
ACCESSION		linear	PAT 16-MAY-2001				
VERSION							
KEYWORDS							
SOURCE							
ORGANISM		Unknown.					
REFERENCE		Unclassified.					
AUTHORS		1 (bases 1 to 17)					
JOURNAL		Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.					
FEATURES		Best Local Similarity 69.2%; Pred. No. 1.5e+05; Matches 9; Conservative 1; Indels 0; Gaps 0;					
source		1. . .17 /organism="unknown"					
BASE COUNT		1 a	5 c	7 g	4 t		
ORIGIN							
QY	4	GGCCUAUCGGUGC 16					
Db	2	GGCCCTGCGGNGC 14					
RESULT 10							
AX010333		AX010333					
LOCUS		Sequence 4 from Patent WO9960007.					
DEFINITION		17 bp DNA					
ACCESSION		linear	PAT 06-SEP-2000				
KEYWORD							
REFERENCE							
AUTHORS		Draper,K.G., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.					
JOURNAL		Intercellular adhesion molecule-1 (ICAM-1) ribozymes Patent: US 583542-A 1998-11-17					
FEATURES		Location/Qualifiers					
source		1. . .17 /organism="unknown"					
BASE COUNT		1 a	5 c	7 g	4 t		
ORIGIN							
QY	4	GGCCUAUCGGUGC 16					
Db	2	GGCCCTGCGGNGC 14					

VERSION	AX010333.1	GT-9997186
KEYWORD	Bacteriophage M13mp18.	
SOURCE	Bacteriophage M13mp18.	
ORGANISM	Viruses.	
REFERENCE	1 (bases 1 to 17)	Unclassified.
AUTHORS	Housby,J.N.	1 (bases 1 to 17)
TITLE	Reagent and method	
JOURNAL	Patent: WO 9960007-A 4 25-NOV-1999;	Lehtovaara,P., Knowles,J., Koivula,A., Bamford,J. and Reinikainen,T.
FEATURES	1.17	A method for complete mutagenesis of nucleic acids
SOURCE	/organism="Bacteriophage M13mp18"	Patent: EP 0285123A2 1 05-OCT-1988;
BASE COUNT	3 a	Location/Qualifiers
ORIGIN	3 a 3 c 9 g 9 9 2 t	1. 17
RESULT 11		
Query Match	62.2%; Score 11.2; DB 6; Length 17;	
LOCUS	Best Local Similarity 68.8%; Pred. No. 2e+05; Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;	
DEFINITION		
ACCESSION	AX215191	
VERSION	Qy 2 AUGGCCAUAGGGGCG 17 Db 1 NAGGGCATTGGGCG 16	
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
FEATURES		
SOURCE		
BASE COUNT		
ORIGIN		
RESULT 13		
Query Match	62.2%; Score 11.2; DB 6; Length 17;	
LOCUS	Best Local Similarity 68.8%; Pred. No. 2e+05; Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;	
DEFINITION		
ACCESSION	AX293459	
VERSION	Qy 2 AUGCCAUAGGGGCG 17 Db 2 AAGGGCATGGTGC 17	
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
FEATURES		
SOURCE		
BASE COUNT		
ORIGIN		
RESULT 14		
Query Match	60.0%; Score 10.8; DB 6; Length 20;	
LOCUS	Best Local Similarity 71.4%; Pred. No. 3.4e+05; Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;	
DEFINITION		
ACCESSION	AX189338	
VERSION	Qy 2 AUGGCCAUAGGGG 15 Db 1 ACGGCTAACGGTG 14	
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
FEATURES		
SOURCE		
BASE COUNT		
ORIGIN		
RESULT 12		
Query Match	62.2%; Score 11.2; DB 6; Length 17;	
LOCUS	Best Local Similarity 56.2%; Pred. No. 2e+05; Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;	
DEFINITION		
ACCESSION	Qy 1 AUUGCCAUAGGGG 16 Db 1 AATGATCTATCTGTGC 1	
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
FEATURES		
SOURCE		
BASE COUNT		
ORIGIN		

BASE COUNT 5 a /note="Primer"
 ORIGIN 5 c 4 g 4 t

Query Match 58.9%; Score 10.6; DB 6; Length 18;
 Best Local Similarity 58.8%; Pred. No. 4.4e+05;
 Matches 10; Conservative 3; Mismatches 4;
 QY 2 AUGGCCUAUCGGUGCGA 18
 Db 17 AAGGCTTATGGGGCCA 1

RESULT 15

AR063454 AR063454 Sequence 6 from patent US 5846705. 20 bp DNA Linear PAT 29-SEP-1999

DEFINITION AR063454 AR063454.1 GI:5992762

VERSION AR063454.1

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1. (bases 1 to 20)
 AUTHORS Wu, R.-Y., You, L.-R. and Soong, T.-S.
 TITLE Nucleotide sequence of two circular ssDNA associated with banana
 bunchy top virus and method for detection of banana bunchy top
 virus

JOURNAL Patent: US 5846705-A 6 008-DEC-1998;

FEATURES Location/Qualifiers 1..20

BASE COUNT 5 a /organism="unknown"
 ORIGIN 4 c 7 g 4 t

Query Match 58.9%; Score 10.6; DB 6; Length 20;
 Best Local Similarity 58.8%; Pred. No. 4.4e+05;
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 2 AUGGCCUAUCGGUGCGA 18
 Db 2 AAGGCTTATGGGGCCA 18

Search completed: May 22, 2003, 19:36:43
 Job time : 1049.64 secs

PT nucleozymes, for modulating gene expression in a plant, mammalian,
 PT bacterial or fungal cell
 XX
 PS Claim 49; Page 77; 96pp; English.
 CC The invention relates to nucleic acid molecules with endonuclease
 CC activity, which are particularly useful for cleavage of RNA or DNA.
 CC The nucleic acids are used in a pharmaceutical composition and are used
 CC to modulate expression of a gene in a plant, mammalian, bacterial or
 CC fungal cell. They are used to cleave a separate nucleic acid, preferably
 CC RNA. The nucleic acids are used to inhibit gene expression and/or cell
 CC proliferation, and can be used to treat a disease or condition. More
 CC than one nucleic acid can be independently targeted to the same or
 CC different sites in a cell. The nucleic acids may be used to study DNA.
 CC The modifications to the nucleic acids optimises their catalytic activity
 CC and can maintain or enhance their activity. They exhibit a high degree
 CC of specificity for RNA. The present sequence represents the coding
 CC sequence of deoxyribozyme #8 used in the method of the invention.
 XX
 SQ Sequence 18 BP; 4 A; 4 C; 6 G; 4 U; 0 other;

Query Match 100.0%; Score 18; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.63;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAUGGCCUAUCGGGCGA 18
 ||||| :|||||
 Db 1 AAUGGCCUAUCGGGUCCGA 18

RESULT 2

AB195945
 ID AB195945 standard; DNA; 20 BP.

XX
 AC AB195945;
 XX
 DT 16-FEB-2002 (first entry)

DE Capture oligonucleotide zip ID#3032 oligo #9.
 KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 KW ligase detection reaction; LDR; p53; BRCA1; infectious disease;
 KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
 KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
 KW environmental monitoring; food industry; feed industry; ss.
 OS Synthetic.
 XX
 WO200179548-A2.

XX
 PD 25-OCT-2001.
 XX
 PP 04-APR-2001; 2001WO-US10958.

PR 14-APR-2000; 2000US-197271P.
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
 DR WPI; 2002-034366/04.

XX
 CC The present invention describes a method (M1) for designing capture
 CC complementary oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridise with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
 XX Example 5; Fig 29; 300pp; English.

CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphotrophic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and bracculus
 CC medensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. AB182074 to
 CC AB197545 represent oligonucleotide sequences used in the exemplification
 CC of the present invention.

XX Sequence 20 BP; 2 A; 6 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 18; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.63;

Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 AUGGCCUAUCGGGCG 17
 ||||| :|||||
 Db 2 ACGGCTTATCGGRCG 17

RESULT 3

AB193941
 ID AB193941 standard; DNA; 20 BP.

XX
 AC AB193941;
 XX
 DT 16-FEB-2002 (first entry)

DE Capture oligonucleotide zip ID#1028 oligo #9.
 KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 KW ligase detection reaction; LDR; p53; BRCA1; infectious disease;
 KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
 KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
 KW environmental monitoring; food industry; feed industry; ss.
 OS Synthetic.
 XX
 WO200179548-A2.

XX
 PD 25-OCT-2001.
 XX
 PP 04-APR-2001; 2001WO-US10958.

PR 14-APR-2000; 2000US-197271P.
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
 XX
 DR WPI; 2002-034366/04.

XX
 CC The present invention describes a method (M1) for designing capture
 CC complementary oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridise with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
 XX Example 5; Fig 29; 300pp; English.

CC The present invention describes a method (M1) for designing capture
 CC complementary oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridise with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal

CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus; viruses e.g. T-cell lymphocytotrophis virus,
 CC Epstein-Barr virus and Polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medinensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. ABI82074 to
 CC ABI07546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention.

SQ Sequence 20 BP; 7 A; 6 C; 4 G; 3 T; 0 other;

Query Match	Score	DB	Length	Pred.	No.	Matches	Local Similarity	Conservative	Mismatches	Indels	Gaps
QY	2	AUGGCCUAUCGGGCGA	18	1.6e+03	3	3	64.7%	64.7%	0	0	0
Db	3	ATGACCAATCGATGCGA	19								

RESULT 4

ID	AA94010 standard; DNA; 20 BP.
XX	AA94010;
AC	
XX	
DT	13-SEP-1999 (first entry)
XX	
DE	PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX	
KW	Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW	sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW	vaccine; neutralising epitope; PCR primer; ss.
XX	
OS	Synthetic.
OS	
XX	Chlamydia pneumoniae.
PN	W09927105-A2.
XX	
PD	03-JUN-1999.
XX	
PF	20-NOV-1998; 98WO-IB01890.
XX	
PR	04-NOV-1998; 98US-0107078.
PR	21-NOV-1997; 97FR-0014673.
XX	
PA	{GEST} GENSET.
XX	
PI	Griffais R;
XX	
DR	WPI; 1999-357842/30.
XX	
PT	Genome sequence of Chlamydia pneumoniae
XX	
PS	Page 1636; Disclosure; 1912pp; English.
XX	

CC AAX91991-X97517 represent PCR primers used to amplify open reading
 CC frames and other nucleic acid sequences from the genome of
 CC Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory
 CC disease such as pneumonia and bronchitis and is thought to be a
 CC contributing factor in heart disease, sarcoidosis, sinusitis, purulent
 CC otitis media, erythema nodosum or pharyngitis. The polypeptides encoded
 CC by the open reading frames of the C. pneumoniae genome (see AAY34584-
 CC AAV35879) can be used in immunogenic compositions as vaccines. Vectors
 CC containing C. pneumoniae nucleotides sequences can also be used as
 CC immunogenic compositions, especially where the vector directs the
 CC expression of a neutralising epitope of C. pneumoniae.

SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 other;

Query Match	Score	DB	Length	Pred.	No.	Matches	Local Similarity	Conservative	Mismatches	Indels	Gaps
QY	1	AAUGGCCUAUCGGUG	15	2.8e+03	3	10	66.7%	66.7%	2	0	0
Db	20	AAAGGCTAACCATG	6								

RESULT 5

ID	AAZ44197 standard; DNA; 20 BP.										
XX	AAZ44197;										
AC											
XX											
DT	24-MAR-2000 (first entry)										
XX											
DE	Marine cerebral nerve tissue differentiation DNA primer SAI.										
XX											
KW	Cerebral nerve tissue differentiation; murine; treatment; primer;										
KW	cerebral nerve disease; ss.										
XX											
OS	Mus sp.										
PN	JP11318468-A.										
XX											
PD	24-NOV-1999.										
XX											
PF	15-MAY-1998; 98JP-0152027.										
XX											
PR	15-MAY-1998; 98JP-0152027.										
XX											
PA	{KANA-} ZH KANAGAWA KAGAKU GIJUTSU ACAD.										
PA	{MEIP } MEIJI MILK PROD CO LTD.										
XX											
DR	WPI; 2000-990527/08.										
XX											
PT	A new protein participating in the differentiation of cerebral nerve tissue										
PT	cell - for the prevention and treatment of cerebral nerve tissue										
XX											
PS	Example 4; Page 13; 22pp; Japanese.										
XX											
CC	This invention describes a novel murine protein which is capable of CC inducing the differentiation of cerebral nerve tissue. The protein and CC the gene are expected to be used for the prevention and the treatment CC of cerebral nerve diseases. AAZ44193-Z44202 represent primers used in CC the isolation of the cerebral nerve tissue differentiation associated CC protein described in the method of the invention.										
XX											
SQ	Sequence 20 BP; 7 A; 7 C; 4 G; 2 T; 0 other;										
Query Match	65.6%	Score	11.8	DB	21	Length	20				
Best Local Similarity	60.0%	Pred.	No.	2.8e+03	4	Mismatches	2	Indels	0	Gaps	0
Matches	9	Conservative									
QY	3	UGGCCUAUCGGUGG	17								
Db	20	TGGTCCTCGGTGCG	6								

RESULT 6

ID	AB193134 standard; DNA; 20 BP.
XX	AB193134
AC	AB193134;
XX	

DT 15-FEB-2002 (first entry)
 XX
 DE Capture oligonucleotide zip IN#221 oligo #9.
 XX
 KW Human; K-ras; PCR primer; probe; capture probe; mutation detection; ligase detection reaction; LDR; P53; BRCA1; BRCA2; infectious disease; infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer; oncogene; tumour suppressor; human papillomavirus; forensic; environmental monitoring; food industry; feed industry; ss. OS Synthetic.
 XX
 PN WO200179548-A2.
 XX
 PD 25-OCT-2001.
 XX
 PR 04-APR-2001; 2001WO-US10958.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
 XX
 DR WPI; 2002-034366/04.
 XX
 PT Designing capture oligonucleotide probes for use on a support to which complementary oligonucleotides hybridize with little mismatch -
 XX
 PS Example 5; Fig 29; 300pp; English.
 The present invention describes a method (M1) for designing capture oligonucleotide probes, (I) for use on a support to which complementary oligonucleotides, (II) will hybridise with little mismatch where (I) have melting temperatures within a narrow range. The method is useful for detecting infectious diseases caused by bacterial infectious agents e.g. *Salmonella*, *Listeria* monocytes and *Haemophilus influenza*, fungal infectious agents e.g. *Cryptococcus neoformans*, *Candida albicans* and *Aspergillus fumigatus*, viruses e.g. T-cell lymphocytotropic virus, Epstein-Barr virus and polio virus, and parasitic infectious agents selected from *Onchocerca volvulus*, *Entamoeba histolytica* and *Draunculus medinensis*. The method is also useful for detecting genetic diseases such as 21 hydroxylase deficiency, Turner Syndrome and obesity defects. Detecting cancer involving oncogenes, tumour suppressor genes, or genes involved in DNA amplification, replication, recombination or repair, the cancer is specifically associated with a gene selected from BRCA1 gene, p53 gene, human papillomavirus types 16 and 18 and liver cancers. The method is also used for environmental monitoring, forensics and the food and feed industry, detecting comprises scanning (using e.g. a scanning electron microscope and infrared microscope) the support at the particular sites and identifying if ligation of the oligonucleotide probe sets occurred and correlating (using a computer) identified ligation to a presence or absence of the target nucleotide sequences. ABI2074 to ABI9756 represent oligonucleotide sequences used in the exemplification of the present invention.

Sequence 20 BP; 1 A; 6 C; 6 G; 7 T; 0 other;

Query Match Best Local Similarity 65.5%; Score 11.8; DB 24; Length 20; Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 UGGCUAUCGGUGCC
 XX :| |::| |::|:
 DB 6 TCCCCATCTGCGC

RESULT 7
 XX AT53656
 ID AT53656 standard; RNA; 17 BP.
 XX AC AT53656;
 CC

DT 27-MAR-1997 (first entry)
 XX
 DE Rat ICAM hammerhead ribozyme target sequence (nt. position 2341).
 XX
 KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS; ss.
 XX
 OS Rattus rattus.
 XX
 PR WO9523225-A2.
 XX
 PD 31-AUG-1995.
 XX
 PR 23-FEB-1995; 95WO-1B00156.
 XX
 PR 30-JAN-1995; 95US-0380734.
 PR 23-FEB-1994; 94US-0201109.
 PR 29-MAR-1994; 94US-0218934.
 PR 04-APR-1994; 94US-0222795.
 PR 07-APR-1994; 94US-0224483.
 PR 15-APR-1994; 94US-0227958.
 PR 15-APR-1994; 94US-022801.
 PR 18-MAY-1994; 94US-0245736.
 PR 06-JULY-1994; 94US-0271280.
 PR 15-AUG-1994; 94US-0291932.
 PR 16-AUG-1994; 94US-0291433.
 PR 17-AUG-1994; 94US-0295620.
 PR 19-AUG-1994; 94US-0295520.
 PR 02-SEP-1994; 94US-0291932.
 PR 08-SEP-1994; 94US-0300039.
 PR 23-SEP-1994; 94US-0311486.
 PR 23-SEP-1994; 94US-0311749.
 PR 28-SEP-1994; 94US-0314397.
 PR 03-OCT-1994; 94US-0316771.
 PR 07-OCT-1994; 94US-0319492.
 PR 11-OCT-1994; 94US-0321993.
 PR 04-NOV-1994; 94US-0348477.
 PR 10-NOV-1994; 94US-0337608.
 PR 28-NOV-1994; 94US-0345516.
 PR 16-DEC-1994; 94US-0357577.
 PR 23-DEC-1994; 94US-0363233.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Stinchcomb DT, Chovira B, Durenzo A, Draper KG, Dudycz LW; Grimm S, Karpejs A, Kisich K, Matulic-Adamic J; McSwiggen JA, Modak A, Pavco P, Beigelman L, Sullivan SM; Sweeder D, Thompson JD, Tracz D, Usman N, Wincott FE; PI Woolf T;
 XX
 DR WPI; 1995-35109/045.
 XX
 PT Ribozymes having modified bases and methods for producing them for use in inhibiting disease related genes
 XX
 PS Claim 2; Page 203; 407pp; English.

The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures, and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and

CC synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the ICAM-1 target sequences and thereby inhibit ICAM-1 expression, making them useful for reducing transplant rejection and alleviating symptoms in patients with rheumatoid arthritis, asthma and other inflammatory disorders.

SQ

Sequence 17 BP; 1 A; 5 C; 7 G; 4 U; 0 other;

Query Match

63.3%; Score 11.4; DB 16; Length 17;

Best Local Similarity

92.3%; Pred. No. 4.7e+03;

Matches

12; Conservative 0; Mismatches 1;

Oy

Indels 0; Gaps 0;

Db

2 GGCCTAUCCGGUGC 14

RESULT 8

AAT53740

AAT53740 standard; RNA; 17 BP.

ID

XX

AC AAT53740;

DT 03-APR-1997 (first entry)

XX

DE Rat ICAM hammerhead ribozyme target sequence (nt. position 2872).
 XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; reI A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome;
 KW AIDS; ss;
 XX OS Rattus rattus.
 XX OS Rattus rattus.
 PN WO9523225-A2.

XX

PD 31-AUG-1995.

XX

PF 23-FEB-1995; 95W0-IB00156.

XX

PR 30-JAN-1995; 95US-0380734.

XX

PR 23-FEB-1994; 94US-0201109.

XX

PR 29-MAR-1994; 94US-0218934.

XX

PR 04-APR-1994; 94US-022795.

XX

PR 07-APR-1994; 94US-0224483.

XX

PR 12-APR-1994; 94US-0227958.

XX

PR 15-APR-1994; 94US-0228041.

XX

PR 18-MAY-1994; 94US-0245736.

XX

PR 06-JUL-1994; 94US-0271280.

XX

PR 16-AUG-1994; 94US-0291932.

XX

PR 17-AUG-1994; 94US-0291433.

XX

PR 19-AUG-1994; 94US-0292620.

XX

PR 02-SEP-1994; 94US-0293520.

XX

PR 08-SEP-1994; 94US-0300000.

XX

PR 23-SEP-1994; 94US-031486.

XX

PR 28-SEP-1994; 94US-0314397.

XX

PR 03-OCT-1994; 94US-0316771.

XX

PR 07-OCT-1994; 94US-0319492.

XX

PR 11-OCT-1994; 94US-0321993.

XX

PR 04-NOV-1994; 94US-0334847.

XX

PR 10-NOV-1994; 94US-0337608.

XX

PR 28-NOV-1994; 94US-0345516.

XX

PR 16-DEC-1994; 94US-0357577.

XX

PR 23-DEC-1994; 94US-0363233.

(RIBO-) RIBOZYME PHARM INC.

Stinchcomb DT, Chowrira B, DiRenzo A, Draper KG, Dudycz LW;

Grimm S, Karpeki A, Kisich K, Matulic-Adamic J;

McSwiggen JA, Modak A, Pavco P, Beigelman L, Sullivan SM;

Sweedler D, Thompson JD, Tracz D, Usman N, Wincott FE;

Woolf T;

WPI; 1995-351090/45.

PT Ribozymes having modified bases and methods for producing them

for use in inhibiting disease related genes

PS claim 2; Page 204, 407pp; English.

The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the ICAM-1 target sequences and thereby inhibit ICAM-1 expression, making them useful for reducing transplant rejection and alleviating symptoms in patients with rheumatoid arthritis, asthma and other inflammatory disorders.

SQ Sequence 17 BP; 1 A; 5 C; 7 G; 4 U; 0 other;

Query Match 63.3%; Score 11.4; DB 16; Length 17;

Best Local Similarity 92.3%; Pred. No. 4.7e+03;

Matches 12; Conservative 0; Mismatches 1;

Oy Indels 0; Gaps 0;

Db 2 GGCCTAUCCGGUGC 14

RESULT 9

AAF02004/c

ID AAF02004

XX AAF02004;

DT 16-FEB-2001 (first entry)

XX DE

Hammerhead ribozyme substrate #299.

XX KW

Ribozyme; erythropoietin; granulocyte colony stimulating factor;

KW

interferon alpha; ss.

XX OS

Homo sapiens.

XX PN

WO200061729-A2.

XX PR

19-OCT-2000.

XX PF

11-APR-2000; 2000WO-US09721.

XX PR

12-APR-1999; 99US-0129390.

XX PA

(RIBO-) RIBOZYME PHARM INC.

XX PI

Blatt L, Zwick M, Pavco P, McSwiggen J;

XX DR

WPI; 2000-647423-62.

XX PT

Enzymatic and antisense nucleic acid inhibition of repressor genes,

PT useful for producing e.g. granulocyte colony stimulating

protein, interferon alpha and erythropoietin -

protein, interferon alpha and erythropoietin

PS Claim 37; Page 62; 164pp; English.

CC The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COU-TF-1, the GATA transcription factor gene, IRF-2 and/or the CATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha.

CC Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 other;

SQ Db 16 TGGCCUAGGGUGGCA 1

RESULT 10

Query Match 62.2%; Score 11.2; DB 21; Length 17;

Best Local Similarity 62.5%; Pred. No. 6.1e+03;

Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 UGGCCUAGGGUGGCA 18

Db 16 TGGCCUAGGGUGGCA 1

RESULT 11

Query Match 62.2%; Score 11.2; DB 21; Length 17;

Best Local Similarity 68.8%; Pred. No. 6.1e+03;

Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUGGCUCAUUGGGUGGC 17

Db 1 AAGGGCGATCAGGTCG 16

XX Human NOGO Hammerhead Ribozyme #633.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNazyme; inozyme; cleaver; ambrizyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; Lymphocytic Leukemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO9960007-A2.

XX PD 25-NOV-1999.

XX PF 17-MAY-1999; 99WO-GB01561.

XX PR 15-MAY-1998; 98EP-0303873.

XX PA (ISIS-) ISIS INNOVATION LTD.

XX PI Southern EM, Shchepinov MS, Housby JN, Hamilton AL, Elder JK; DR WPI; 2000-062435/05.

XX PT Analysis of compounds using a solid support, labeled compounds and mass spectrometry

XX PS Example 3; Page 26; 65pp; English.

CC The invention provides new methods for the analysis of compounds, particularly nucleic acids, that use a solid support, labeled compounds and mass spectrometry. A novel method of making a set of labeled compounds, using of a support and a set of labels comprises: (1) at least one first or intermediate step comprising dividing the support into lots, performing a different chemical reaction on each lot of the support so as either to modify that lot of the support or to couple a chemical moiety to that lot of the support, tagging a fraction of each lot of the support with a different label, and combining the lots of the support, and (2) at least one intermediate or final step comprising dividing the support into lots, performing a different chemical reaction on each lot of the support, so as either to modify that lot of the support or to couple a chemical moiety to that lot of the support, tagging a fraction of each lot of the support with a different label, where each different label is linked to a chemical moiety a labeled compound which is separable from the support, and combining the lots of the support. The methods and products are used for the analysis of chemical compounds,

CC particularly nucleic acid molecules.

CC Sequence 17 BP; 3 A; 3 C; 9 G; 2 T; 0 other;

SQ Query Match 62.2%; Score 11.2; DB 21; Length 17;

Best Local Similarity 68.8%; Pred. No. 6.1e+03;

Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUGGCUCAUUGGGUGGC 17

Db 1 AAGGGCGATCAGGTCG 16

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury

XX PS Claim 88; Page 76; 200pp; English.

CC The invention relates to a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNazyme) an inozyme (an endolytic nucleic acid cleaving a an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr an ambrizyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used

CC to cleave RNA of CD20 in the presence of a divalent cation that is
 CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce
 CC CD20 activity of the cell and treat a patient having a condition
 CC associated with the level of CD20. The treatment may further comprise the
 use of one or more therapies. In particular, the CD20 targetting
 nucleic acid may be used to treat lymphoma, leukaemia, B-cell
 lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
 CC low-grade or follicular NHL, lymphocytic leukaemia, HIV (human
 immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
 CC immunoblastic (IMC), small-B-cell lymphocytic lymphoma, immune
 thrombocythaemia, and inflammatory arthropathy. The NOGO-targetting
 CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a
 CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
 CC may be contacted with a cell to reduce NOGO activity of the cell and
 CC treat a patient having a condition associated with the level of NOGO. The
 treatment may further comprise the use of one or more therapies.
 CC In particular, the NOGO-targetting nucleic acid may be used to treat
 CC central nervous system (CNS) injury and cerebrovascular accident (CVA),
 CC stroke, Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The
 present sequence is a hammerhead ribozyme of the invention.

XX SQ Sequence 17 BP; 7 A; 3 C; 3 G; 4 U; 0 other;

Query Match 62.2%; Score 11.2; DB 23; Length 17;
 Best Local Similarity 56.2%; Pred. No. 6.1e+03;
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAUGGCCUAUCGGGUC 16
 Db 16 ATAGTCTAATCTGTGC 1

RESULT 12

ABI93501
 ID ABI93501 standard; DNA; 20 BP.
 XX

AC ABI93501;
 XX

DT 15-FEB-2002 (first entry)

XX DE Capture oligonucleotide zip ID#588 oligo #9.

XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 KW ligase detection reaction; LUR; p53; BRCA2; Infectious disease;
 infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
 KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
 KW environmental monitoring; food industry; feed industry; ss.
 OS Synthetic.
 XX PN WO200179548-A2.

XX PD 25-OCT-2001.
 XX PF 04-APR-2001; 2001WO-US10958.

XX PR 14-APR-2000; 2000US-197271P.
 XX (CORR) CORNELL RES FOUND INC.

XX PT Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
 XX WPI; 2002-03-366/04.

PT Designing capture oligonucleotide probes for use on a support to which
 PT complementary oligonucleotides hybridize with little mismatch -
 XX Example 5; Fig 29; 300pp; English.

CC The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridise with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 for detecting infectious diseases caused by bacterial infections agents
 e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus, cirsis,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents,
 selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 medinensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 method is also used for environmental monitoring, forensics and the food
 and feed industry; detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. AB182074 to
 CC AB197546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention.

XX SQ Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 other;

Query Match 60.0%; Score 10.8; DB 24; Length 20;
 Best Local Similarity 71.4%; Pred. No. 1.1e+04;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 AUGGCCUAUCGGUG 15
 Db 1 ACGGCCTAACGGTG 14

RESULT 13

ADD08688/C
 ID ADD08688 standard; DNA; 18 BP.
 XX

AC ADD08688;
 XX

DT 04-SEP-2001 (first entry)

XX DE Drosophila mus101 genomic and partial cDNA sequencing primer, GENX9P8.

XX KW Mus101; BRCA1 C-Terminus; BRCT; gene therapy; tumour; mitosis inhibitor;
 DNA repair; cell cycle regulation; passive immunotherapy; primer; ss.

XX OS Drosophila sp.
 XX .PN WO200148202-R1.

XX PD 05-JUL-2001.

XX PF 21-DEC-2000; 2000WO-GB04956.
 XX PR 24-DEC-1999; 99GB-0030703.

XX PA (CYCL-) CYCLACEL LTD.

XX PI Glover DM, Yamamoto R, Henderson D;
 XX DR WPI; 2001-418282/44.

XX Novel mus101 polypeptide, a member of BRCT superfamily derived from
 PT Drosophila useful for identifying substance capable of affecting Mus101
 PT function, and for treating tumor
 XX Example; Page 44; 108pp; English.

XX The present sequence is a primer which is used to sequence the
 CC Drosophila mus101 genomic and partial cDNAs. The mus101 is a member of

BRCT (BRCA1 C-Terminus) superfamily. The musl01 polynucleotide probe is used for detecting the presence or absence of musl01 polynucleotide in a biological sample by bringing the biological sample containing DNA or RNA into contact with musl01 polynucleotide probe under hybridising conditions, and detecting any duplex formed between musl01 polynucleotide probe and musl01 polynucleotide in the sample. The musl01 and its polynucleotide are useful in gene therapy. The musl01 is useful for identifying a substance capable of affecting musl01 function, and the substance is useful for treating tumour, for inhibiting mitosis and for increasing the susceptibility of a tumour cell to a DNA damaging agent. The musl01 is also useful for identifying substances which affects DNA repair and cell cycle regulation, in vitro or in vivo cell culture system to study the role of musl01 and its homologues in disease, and as passive immunogens. The antibody to musl01 is useful in diagnosis and in passive immunotherapy. It is also useful for detecting musl01 in a biological sample.

Query Match 58.9%; Score 10.6; DB 24; Length 18;
 Best Local Similarity 58.8%; Pred. No. 1.4e+04;
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Sequence 18 BP; 5 A; 5 C; 4 G; 4 T; 0 other;

Query Match 58.9%; Score 10.6; DB 22; Length 18;
 Best Local Similarity 58.8%; Pred. No. 1.4e+04;
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 AUGGCCUAUCGGUGCGA 18
 Db 18 ATGGCTTACCCAGGGA 2

RESULT 14

ABL41065_c
 ID ABL41065 standard; DNA; 18 BP.
 XX
 AC ABL41065;
 XX
 DT 12-AUG-2002 (first entry)
 XX
 DE 16s rRNA encoding DNA specific probe.
 XX
 KW Microbe; water treatment; 16s rRNA; probe; ss.
 XX
 OS Synthetic.
 XX
 PT Banana bunchy top virus; BBTV; PCR technique; plant; tissue; banana; Musa; phloem damage; aphid; nucleic acid detection; PCR primer; ss.
 XX
 KW Banana bunchy top virus; BBTV; PCR technique; plant; tissue; banana; Musa; phloem damage; aphid; nucleic acid detection; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN U5846705-A.
 XX
 PR 06-APR-1995; 95US-0418071.
 XX
 PD 08-DEC-1998.
 XX
 PF 06-APR-1995; 95US-0418071.
 XX
 PN 06-APR-1995; 95US-0418071.
 XX
 PA (BIOT-) DEV CENT BIOTECHNOLOGY.
 XX
 PI Soong, T.; Wu, R.; You, L.;
 XX
 DR WPI; 1999-059037/05.
 XX
 PS Nucleic acids having banana bunchy top virus component sequences - used to design primers for use in polymerase chain reaction
 XX
 PT detection of the virus
 XX
 C1aim 10; Column 9; 27pp; English.
 XX
 Sequences AAV71835 to AAV71841 represent PCR primers specific for the banana bunchy top virus (BBTV) DNA. The invention provides BBTV DNA I (clone 7-4-2) circular single stranded (css) DNA II (clone 2-17) css DNA sequences (AAV71832 and AAV71833) and the proteins (AAW87459 and AAW87460), encoded by the open reading frames in the nucleotide sequences. The nucleic acid sequences (AAV71830 to AAV71833) are used as the basis for the construction of PCR primers, to detect BBTV infection. The PCR technique is used for detecting BBTV in plant tissues (preferably banana, especially Musa species). The virus, one of the most important banana species viruses, causes phloem damage and is transmitted by aphids. PCR detection gives accurate, reliable and specific determination of absence or presence of the virus.

Sequence 20 BP; 5 A; 4 C; 7 G; 4 T; 0 other;

Query Match 58.9%; Score 10.6; DB 20; Length 20;
 Best Local Similarity 58.8%; Pred. No. 1.4e+04;
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 AUGGCCUAUCGGUGCGA 18
 Db 2 AUGGTCTATCAGGCAA 18

RESULT 15

AAV71835
 ID AAV71835 standard; DNA; 20 BP.
 XX
 AC AAV71835;
 XX
 DT 10-FEB-1999 (first entry)
 XX
 DE Bunchy top banana virus (BBTV) DNA specific primer BB-1.
 XX
 KW Banana bunchy top virus; BBTV; PCR technique; plant; tissue; banana; Musa; phloem damage; aphid; nucleic acid detection; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN U5846705-A.
 XX
 PR 06-APR-1995; 95US-0418071.
 XX
 PD 08-DEC-1998.
 XX
 PF 06-APR-1995; 95US-0418071.
 XX
 PN 06-APR-1995; 95US-0418071.
 XX
 PA (BIOT-) DEV CENT BIOTECHNOLOGY.
 XX
 PI Soong, T.; Wu, R.; You, L.;
 XX
 DR WPI; 1999-059037/05.
 XX
 PS Nucleic acids having banana bunchy top virus component sequences - used to design primers for use in polymerase chain reaction
 XX
 PT detection of the virus
 XX
 C1aim 10; Column 9; 27pp; English.
 XX
 Sequences AAV71835 to AAV71841 represent PCR primers specific for the banana bunchy top virus (BBTV) DNA. The invention provides BBTV DNA I (clone 7-4-2) circular single stranded (css) DNA II (clone 2-17) css DNA sequences (AAV71832 and AAV71833) and the proteins (AAW87459 and AAW87460), encoded by the open reading frames in the nucleotide sequences. The nucleic acid sequences (AAV71830 to AAV71833) are used as the basis for the construction of PCR primers, to detect BBTV infection. The PCR technique is used for detecting BBTV in plant tissues (preferably banana, especially Musa species). The virus, one of the most important banana species viruses, causes phloem damage and is transmitted by aphids. PCR detection gives accurate, reliable and specific determination of absence or presence of the virus.

Sequence 20 BP; 5 A; 4 C; 7 G; 4 T; 0 other;

Query Match 58.9%; Score 10.6; DB 20; Length 20;
 Best Local Similarity 58.8%; Pred. No. 1.4e+04;
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 AUGGCCUAUCGGUGCGA 18
 Db 2 AUGGTCTATCAGGCAA 18

Search completed: May 22, 2003, 19:04:27
 Job time : 178.636 secs

Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 other;

Query Match 58.9%; Score 10.6; DB 24; Length 18;
 Best Local Similarity 64.7%; Pred. No. 1.4e+04;
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Gencore version 5.1.4_p5_4578
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Om nucleic - nucleic search, using sw model

Run on:

May 22, 2003, 18:32:43 ; search time 1311.82 Seconds

(without alignments)

22.225 Million cell updates/sec

Title: US-09-780-929-98

Perfect score: 18

Sequence: 1 aaugggccauacggugcga 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched:

16154066 seqs, 8097743376 residues

Post-processing: Minimum Match 0% Maximum Match 100%

Total number of hits satisfying chosen parameters:

5800

Minimum DB seq length: 0

Maximum DB seq length: 20

Database : EST:*

1: em_estba:*

2: em_estbam:*

3: em_estbin:*

4: em_estml:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_eston:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rnd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
C 1	9.6	53.3	20	A2514794 1M0361C13
C 2	9.2	51.1	20	A2601483 1M0419H15
C 3	8.4	46.7	15	BQ511821 EST619336
C 4	8.2	45.6	19	A2329706 1M0054006
C 5	8.2	45.6	19	A2515014 1M0054006
C 6	8.2	44.4	20	BP966452 602287666

ALIGMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
1	A2514794	20 bp DNA linear GSS 05-OCT-2000	A2514794	1M0361C13R	Mouse 10kb plasmid UGGCLM library Mus musculus genomic clone UGGCLM0361C13 R, DNA sequence.		
			A2514794	A2514794.1	GI:10696610		
					GSS.		
					house mouse.		
					Mus musculus		
					Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
					M (bases 1 to 20)		
					Dunn, D., Royaci, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.		
					Insert Length: 10000 Std Error: 0.00		

REFERENCE Dunn, D., Royaci, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
AUTHORS Contact: Robert B. Weiss
JOURNAL Unpublished (2000)
COMMENT University of Utah Genome Center

FEATURES	source	Plate: 0361 row: C column: 13
FEATURES	source	Seq primer: CACACAGGAACAGCTATGACC
FEATURES	source	Class: plasmid ends
FEATURES	source	High quality sequence stop: 20.
FEATURES	source	Location/Qualifiers
source		1. .20
/organism="Mus musculus"		
/strain="C57BL/6J"		
/db_xref="taxon:10090"		
/clone="UUGCIM0361C13"		
/clone_lib="Mouse 10kb plasmid UUGCIM library"		
/sex="Male"		
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"		
/note="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 Polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptorized mouse DNA was annealed to adaptorized vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."		
BASE COUNT	4 a 6 c 7 g 3 t	ORIGIN
Query Match		
Best Local Similarity	53.3%	Score 9.6; DB 17; Length 20;
Matches	9;	Conservative
QY	2 AUGGCCUAUCGGUGCG	17
Db	17 ATGGCCACTGGTCCG	2
RESULT 2		
AZ601483/c		
LOCUS	AZ601483	20 bp DNA, linear GSS 13-DEC-2000
DEFINITION	1M019H15R Mouse 10kb plasmid UUGCIM library MUS musculus genomic clone UUGCIM0419H15 R, DNA sequence.	
ACCESSION	AZ601483	
VERSION	AZ601483.1	GI:11723673
KEYWORDS		GSS.
SOURCE		house mouse.
ORGANISM	MUS musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenah,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts	
TITLE	Unpublished (2000)	
JOURNAL	Contact: Robert B. Weiss	
COMMENT	University of Utah Genome Center	
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA	
	Tel: 801 585 5606	
	Fax: 801 585 7177	
	Email: ddunne@genetics.utah.edu	
	Insert length: 10000 Std Error: 0.00	
BASE COUNT	3 a 6 c 7 g 4 t	ORIGIN
Query Match		
Best Local Similarity	51.1%	Score 9.2; DB 17; Length 20;
Matches	9;	Conservative
QY	3 UGGCCUAUGGGUC	16
Db	19 TGGCCAACAGTGCG	6
RESULT 3		
BQ511821		
LOCUS	BQ511821	15 bp mRNA, linear EST 10-JUN-2002
DEFINITION	BQ511821 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone STMHU18 5 end, mRNA sequence.	
ACCESSION	BQ511821	
VERSION	BQ511821.1	GI:21370690
KEYWORDS		EST.
SOURCE		Potato.
ORGANISM		Solanum tuberosum
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; Asteridae; eudicots I; Solanales; Solanaceae; Solanum.	
AUTHORS	Buell,C.R., Hart,A., Baker,B., Tankley,S., Fry,W., Smart,C., Restrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and Karaycheva,S.A.	
TITLE	Generation of a set of potato cDNA clones for microarray analyses Unpublished (2002)	
JOURNAL	Contact: Robin Buell	
COMMENT	The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Email: potato@tigr.org	
	This clone is available through the Research Genetics contact the Research Genetics for further information 1-800-711-6195 or concaregen.com	
	Seq primer: T3.	

FEATURES	source	location/Qualifiers
	0.15	0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA Polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWPA2 (gi 4732114gb AT129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.
BASE COUNT	3 a 5 c 5 t	tubers or roots." ORIGIN
ORIGIN		
Query Match	46.7%; Score 8.4; DB 14; Length 15;	
Best Local Similarity	60.0%; Pred. No. 2.3e+06;	
Matches	6; Conservative	
DEFINITION	3; Mismatches	
QY	1 AAUGGCCUAU 10	
Db	5 AATGGCCTCT 14	
RESULT 4	AZ329705/C	
LOCUS	AZ329705	19 bp DNA linear GSS 29-SEP-2000
DEFINITION	IM0054D06R Mouse 10kb plasmid UGGC1M library Mus musculus genomic clone UGGC1M0054D06 R, DNA sequence.	
ACCESSION	AZ329705	
VERSION	AZ329705.1	
KEYWORDS	GI:10390686	
SOURCE	GSS.	
ORGANISM	Mus musculus	
REFERENCE	Dunn, D., Avogadro, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.	
AUTHORS	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	
JOURNAL	Unpublished (2000)	
COMMENT	Contact: Robert B. Weiss	
TITLE	University of Utah Genome Center	
JOURNAL	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA	
COMMENT	Fax: 801 585 5605	
COMMENT	Email: dunn@genetics.utah.edu	
FEATURES	Insert Length: 10000	
source	Plate: 0054 row: D column: 06	
source	Seq primer: CACAGGGAAACGCGATGACC	
source	Class: plasmid ends	
source	High quality sequence stop: 19.	
source	Location/Qualifiers	
source	1..19	
/organism="Mus musculus"		
/strain="C57BL/6J"		
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/clone="UGGC1M0054D06"		
/sex="Male"		
/lab_host="E. coli strain X110-Gold, T1-resistant, F-"		
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.Jax.org/resources/documents/dnare/). The DNA		
RESULT 5	AZ151014/C	
LOCUS	AZ151014	19 bp DNA linear GSS 05-OCT-2000
DEFINITION	IM0054D06F Mouse 10kb plasmid UGGC1M library Mus musculus genomic clone UGGC1M0054D06 F, DNA sequence.	
ACCESSION	AZ151014	
VERSION	AZ151014.1	
KEYWORDS	GI:10696330	
SOURCE	GSS.	
ORGANISM	Mus musculus	
REFERENCE	Dunn, D., Royagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.	
AUTHORS	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	
JOURNAL	Unpublished (2000)	
COMMENT	Contact: Robert B. Weiss	
TITLE	University of Utah Genome Center	
JOURNAL	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA	
COMMENT	Fax: 801 585 5606	
COMMENT	Email: dunn@genetics.utah.edu	
FEATURES	Insert Length: 10000	
source	Plate: 0054 row: D column: 06	
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source	Class: plasmid ends	
source	High quality sequence stop: 19.	
source	Location/Qualifiers	
source	1..19	
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/clone="UGGC1M0054D06"		
/sex="Male"		
/lab_host="E. coli strain X110-Gold, T1-resistant, F-"		
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.Jax.org/resources/documents/dnare/). The DNA		

Page 4

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (91147321141gb) AF12072.1, a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adopted vector DNA, and transformed into

BASE COUNT and selected for ampicillin resistance.^a

Qy	4	GGCCUAUCGAGC	16
	: :		
Rv	17	GGCCUAUCGAGC	16

RESULT 6
BF966452
LOCUS BF966452 20 bp mRNA linear EST 23-JAN-2001
DEFINITION 60228706-F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:43756485,
ACCESSION mRNA sequence.
BF966452
VERSION 1
~~PROCESSED~~ 3 671200052

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

 ESR.
 human.
Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 20)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 On Jan 16, 2001 this sequence version replaced g1:1233367.

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Caninici (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LUM0041 **row:** d **column:** 17
High sequence stop: 20.

source

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/db_xref="taxon:9606"
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/lab_host="DH10B"
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ORIGIN					
RESULT	7				
LOCUS	BQ750930/c				
DEFINITION	EST631493 dsCT Colletotrichum trifolii	12 bp	mRNA	linear	EST 18-JUL-2002
ACCESSION	BQ750930		sequence.		
VERSION	BQ750930.1				
KEYWORDS	EST.				
SOURCE					
ORGANISM	Colletotrichum trifolii				
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariidae; Incertae sedis; Phyllochloraceae; mitosporic Phyllochloraceae; Colletotrichum.				
AUTHORS	1 (bases 1 to 12) Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Utterback, T., Cheung, F., and Fraser, C.M.				
TITLE	ESTs from mycelia of Colletotrichum trifolii race 1				
JOURNAL	Unpublished (2002)				
COMMENT	Other ESTs: EST631492				
Contact:	Deborah A. Samac				
Department of Plant Pathology					
University of Minnesota					
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA					
Tel:	612 625 1243				
Fax:	651 649 5053				
Email:	debbys@puccini.crl.umn.edu				
TIGR sequence name:	MTSA5TIV				
www.medicago.org	More information is available at:				
Seq primer:	(gtA ATA CGA CTC ACT ATA ggg C).				
FEATURES	Location/Qualifiers				
source					
	1..12				
/organism="Colletotrichum trifolii"					
/strain="race 1"					
/db_xref="taxon:5166"					
/clone="PDST1-51"					
/clone_id="DSCT1-51"					
/tissue_type="mycelia"					
/dev_stage="young", actively growing mycelia (3 days after inoculation) grown in liquid culture (cotton minimal medium containing 2%glucose)."					
/lab_host="DH5alpha"					
/note="vector: pBluescript SK+; site_1: EcoRI; site_2:					
ECORI; isolate: 2502 ; CDNA was prepared from polyA+					
enriched RNA. The cDNA was ligated into Lambda gtlf from Stratagene and packaged using Gigapack packaging extracts.					
An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."					
BASE COUNT	5 a	3 c	4 g	0 t	
ORIGIN					

Db	12 GGCCTTCGTT	2
RESULT	8	
REFERENCE	BM39285	
LOCUS	BM39285	18 bp mRNA linear EST 17-JAN-2002
DEFINITION	5009-0-2-A10.t.1 Chilcoat/Turkewitz cDNA, mRNA sequence.	
ACCESSION	BM39285	
VERSION	BM39285.1	GI:18196338
KEYWORDS	EST.	
SOURCE	Tetrahymena thermophila.	
ORGANISM	Tetrahymena thermophila.	
FEATURES		
source	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena; 1 (bases 1 to 18)	
FEATURES		
source	Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel , J., and Klobutcher, L.A. EST from Tetrahymena thermophila, strain CU428.1, growing cells Unpublished (2002) Contact: Turkewitz AP Molecular Genetics and Cell Biology University of Chicago 920 E. 58th Street, Chicago, IL 60637, USA Tel: 773 702 4374 Fax: 773 702 3172 Email: apturkew@midway.uchicago.edu Seq primer: T3.	
FEATURES		
source	Location/Qualifiers 1..18 /organism="Tetrahymena thermophila" /strain="C428.1" /db_xref="taxon:10090" /clone="UUGCCTM0034A07"	
FEATURES		
source	/clone.lib="Mouse 10kb plasmid UUGCIM library" /sex="Male" /lab_host="E. coli strain XL10-Gold, TI-resistant, F- " /note="vector: pMD42uv; Purified genomic DNA from M. musculus C5BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.Jax.org/resources/documents/shares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g11473149b; AF129072). A copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	
BASE COUNT	3 a 3 c 8 g 4 t	
ORIGIN		
RESULT	9	
LOCUS	AZ787588/C	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M0034A07F Mouse 10kb Plasmid UGGCIM library Mus musculus genomic clone UUGC2M0034A07 F, DNA sequence.	
ACCESSION	AZ787588	
VERSION	AZ787588.1	GI:12926329
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	10	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	11	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	12	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	13	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	14	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	15	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	16	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	17	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	18	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	19	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	20	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	21	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	22	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	23	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	24	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	25	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	26	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	27	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	28	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	29	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	30	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	31	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	32	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	33	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	34	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	35	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	36	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	37	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	38	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	39	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	40	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	41	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	42	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	43	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	44	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	45	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	GI:12952969
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
RESULT	46	
LOCUS	AZ800646	19 bp DNA linear GSS 16-PERB-2001
DEFINITION	2M005814R Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UUGC2M0058H14 R, DNA sequence.	
ACCESSION	AZ800646	
VERSION	AZ800646.1	

FEATURES	source	High quality sequence stop: 19.
		Location/Qualifiers
	1. .19	
		/organism="Mus musculus"
		/strain="C57BL/6J"
		/db_xref="taxon:10090"
		/clone="UUGC2M058H14"
		/clone_id="Mouse 10kb plasmid UGGC1M library"
		/sex="Male"
		/note="Vector: PWD4Inv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.Jax.org/resources/documents/dnarecs/). The DNA was hydrodynamically sheared by repeated passage through a lab host="E. coli strain XL10-Gold, T1-resistant, F-"
		/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
		/note="Vector: PWD4Inv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.Jax.org/resources/documents/dnarecs/). The DNA was hydrodynamically sheared by repeated passage through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi 47321149 AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT	3 a 4 c 7 g 5 t	
ORIGIN		
RESULT 11		
LOCUS	AZ779244/	20 bp DNA linear GSS 16-FEB-2001
DEFINITION	2M0015119F Mouse 10kb plasmid UGGC1M library Mus musculus genomic clone UGGC2M0015119 F, DNA sequence.	
ACCESSION	AZ779244	
VERSION	AZ779244.1	GI:12909701
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	Dunn D., Hoyng, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenem, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.	
AUTHORS	and Wright, D., Weiss, R.	
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	
JOURNAL	Unpublished (2000)	
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT	
FEATURES	source	High quality sequence stop: 20.
		Location/Qualifiers
	1. .20	
		/organism="Mus musculus"
		/strain="C57BL/6J"
		/db_xref="taxon:10090"
		/clone="UUGC2M05119"
		/clone_id="Mouse 10kb plasmid UGGC1M library"
		/sex="Male"
		/note="Vector: PWD4Inv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.Jax.org/resources/documents/dnarecs/). The DNA was hydrodynamically sheared by repeated passage through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi 47321149 AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT	3 a 4 c 7 g 5 t	
ORIGIN		
RESULT 12		
LOCUS	HSMC21G06	20 bp DNA linear GSS 29-MAY-1997
DEFINITION	H.sapiens DNA for trapped exon (ID HMC21G06), genomic survey sequence.	
ACCESSION	X88286	
VERSION	X88286.1	GI:1437772
KEYWORDS	GSS.	
SOURCE	Hom sapiens.	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 20)	
AUTHORS	Chen, H.M., Rossier, C., Chrast, R. and Antonarakis, S.E.	
TITLE	Cloning of trapped exons from human chromosome 21.	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 20)	
AUTHORS	Antonarakis, S.E.	
TITLE	Direct Submission	
JOURNAL	Submitted (17-MAR-1995)	
REFERENCE	1 Michel-Servet, 1211 Geneva, SWITZERLAND	
AUTHORS	Chen, H., Chrast, R., Rossier, C., Morris, M.A., Lalioti, M.D. and	

TITLE	Antonarakis,S.E.
JOURNAL	Cloning of 559 potential exons of genes of human chromosome 21 by exon trapping
MEDLINE	Genome Res. 6 (8), 747-760 (1996)
PUBMED	97011340
FEATURES	Location/Qualifiers
source	1..20
/organism="Homo sapiens"	
/ab_xref="taxon:9606"	
exon	1..20
/note="trapped exon"	
BASE COUNT	5 a 5 c 5 g 4 t 1 others
ORIGIN	
Query Match	Score 43.3%; DB 17; Length 20;
Best Local Similarity 58.3%; Pred. No. 4_9e+06; Mismatches 3; Indels 0; Gaps 0;	Matches 7; Conservative
QY	7 CUAUCCGGGCGA 18
1:1 1:1 1:1 1:1	
Db	4 CTACCGGNGTGA 15
RESULT 13	
LOCUS	BM394638
DEFINITION	50072-2-5-B10.r.1 Chilcoat/Turkewitz cDNA (large fraction)
ACCESSION	BM394638
VERSION	BM394638.1
VERSIONS	EST
SOURCE	Tetrahymena thermophila.
ORGANISM	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE	1 (bases 1 to 18)
AUTHORS	Turkewitz,A.P., Karrer,K.M., Jahn,C., Orrias,E., Kirk,K.E., Frankel,J., and Kloibocher,L.
TITLE	EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL	Unpublished (2002)
COMMENT	Contact: Turkewitz AP Molecular Genetics and Cell Biology University of Chicago 920 E. 58th Street, Chicago, IL 60637, USA Tel: 773 702 4374 Fax: 773 702 3172 Email: apturkewitz@midway.uchicago.edu
FEATURES	Seq primer: T3.
source	Location/Qualifiers
1..18	
/organism="Homo sapiens"	
/ab_xref="taxon:9606"	
/clone="IMAGE:150217"	
/tissue="carcinoid"	
/clone_type="carcinoid"	
/ab_host="DH10B"	
/note="Organ: lung; Vector: PT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoma and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified PT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."	
BASE COUNT	5 a 4 c 6 g 4 t
ORIGIN	
Query Match	Score 42.2%; DB 13; Length 18;
Best Local Similarity 57.1%; Pred. No. 6e+06; Mismatches 8; Conservative	Matches 8; Conservative
QY	2 AUGGCCUAUCCGGUG 15
1:1 1:1 1:1 1:1	
Db	2 ATGGCAGCGGGTG 15
RESULT 14	
Query Match	Score 42.2%; DB 13; Length 19;
Best Local Similarity 57.1%; Pred. No. 6e+06; Mismatches 8; Conservative	Matches 8; Conservative
BASE COUNT	3 a 3 c 10 g. 2 t
ORIGIN	
Query Match	Score 42.2%; DB 13; Length 19;
Best Local Similarity 57.1%; Pred. No. 6e+06; Mismatches 8; Conservative	Matches 8; Conservative
QY	1 AUAGGCCUAUCCGGU 14
1:1 1:1 1:1 1:1	
Db	1 ATATAGCCAGGGGT 14
RESULT 15	
LOCUS	A1625518
DEFINITION	ty5qd06 xl NCI-CGAP_Lu5 Homo sapiens cDNA clone IMAGE:2283083 3'
ACCESSION	A1625518
similar to TR_P93237_P9237 PROLINE-RICH PROTEIN PRP2 PRECURSOR.	
;contains MSRI.t1 MSRI repetitive element ; mRNA sequence.	

VERSION A1625518.1 GI:4650449
 KEYWORDS EST
 SOURCE human
 ORGANISM Homo sapiens
 REFERENCE 1
 AUTHORS NCI-CGAP (bases 1 to 19)
 TITLE NCI-CGAP http://www.nci.nlm.nih.gov/ncicgap.
 Tumor Gene Index
 unpublished (1997)
 JOURNAL COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 DNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Seq primer: -400P from Gibco
 High quality sequence stop: 1.

FEATURES source
 /location/qualifiers
 1. 19
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2283083"
 /clone_id="NCI CGAP UT2"
 /tissue_type="moderately-differentiated endometrial
 adenocarcinoma, 3 pooled tumors"
 /lab_host="DHIOB"
 /note="Organ: uterus; Vector: pCMV-SPORT5; Site_1: Sall;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.85 kb. Life Technologies catalog #:
 11539-012"
 BASE COUNT
 ORIGIN
 Query Match 42.2%; Score 7.6; DB 9; Length 19;
 Best Local Similarity 50.0%; Pred. No. 6e+06;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; gaps 0;
 Qv 4 GGCCTAUCGGUGCG 17
 || : : 11-111
 Db 19 GGGTTTGGGGCG 6

Search completed: May 22, 2003, 20:17:07.
 Job time : 1317.82 secs

GenCore version 5.1.4_p5_4578
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Om nucleic - nucleic search, using sw model

Run on: May 22, 2003, 18:55:07 ; Search time 38.7273 Seconds
(without alignments)
142.540 Million cell updates/sec

Title: US-09-780-929-98

Perfect score: 18
Sequence: 1 aaugggccauacggugcgca 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA: *
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/9CTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11.4	63.3	17	2 US-09-292-620A-1886	Sequence 1886, Appl
2	11.4	63.3	17	2 US-09-292-620A-1977	Sequence 1977, Appl
3	11.4	63.3	17	3 US-09-071-8451-1886	Sequence 1886, Appl
4	11.4	63.3	17	3 US-09-071-8451-1977	Sequence 1977, Appl
5	10.6	58.9	20	2 US-09-418-071-6	Sequence 6, Appl
6	10.4	57.8	15	1 US-08-182-968A-497	Sequence 497, Appl
7	10.4	57.8	15	2 US-08-374-306A-497	Sequence 497, Appl
8	10.4	57.8	15	3 US-08-064-156A-497	Sequence 5, Appl
9	10.2	56.7	15	3 US-09-059-779-5	Sequence 5815, APPL
10	10.2	56.7	17	4 US-09-584-040-5815	Sequence 5815, APPL
11	10.2	56.7	17	4 US-08-584-040-5816	Sequence 5817, APPL
12	10.2	56.7	17	4 US-08-584-040-5817	Sequence 5817, APPL
13	10.2	56.7	18	2 US-08-108-837-3	Sequence 3, APPL
14	10	55.6	12	3 US-08-948-097-7	Sequence 7, APPL
15	10	55.6	20	1 US-08-222-177A-108	Sequence 108, APPL
16	9.8	54.4	16	3 US-08-872-917-11	Sequence 11, APPL
17	9.8	54.4	17	4 US-08-584-040-5814	Sequence 5814, APPL
18	9.8	54.4	20	4 US-08-837-201C-66	Sequence 66, APPL
19	9.8	54.4	20	4 US-09-364-416-66	Sequence 66, APPL
20	9.6	53.3	17	4 US-08-584-040-7863	Sequence 7863, APPL
21	9.6	53.3	17	4 US-08-679-645-264	Sequence 264, APPL
22	9.6	53.3	18	3 US-09-143-212-60	Sequence 60, APPL
23	9.6	53.3	18	4 US-08-679-645-643	Sequence 643, APPL
24	9.6	53.3	19	1 US-07-794-401-16	Sequence 16, APPL
25	9.6	53.3	19	1 US-08-397-470-16	Sequence 11, APPL
26	9.6	53.3	20	1 US-08-356-405-11	Sequence 66, APPL

247290

ALIGNMENTS

c	28	9.6	53.3	20	2 US-08-488-177-66	Sequence 55, APPL
c	29	9.6	53.3	20	2 US-08-664-336-66	Sequence 66, APPL
c	30	9.6	53.3	20	2 US-08-481-066A-66	Sequence 66, APPL
c	32	9.6	53.3	20	4 US-09-312-930-6	Sequence 6, APPL
c	33	9.6	53.3	20	4 US-08-943-731-546	Sequence 56, APPL
c	34	9.6	53.3	20	4 US-09-593-589-72	Sequence 72, APPL
c	35	9.6	53.3	20	4 US-08-820-637A-66	Sequence 66, APPL
c	36	9.4	52.2	12	4 US-09-281-418-54	Sequence 54, APPL
c	37	9.4	52.2	18	1 US-08-126-560A-30	Sequence 30, APPL
c	38	9.4	52.2	18	2 US-08-465-380-100	Sequence 100, APPL
c	39	9.4	52.2	18	2 US-08-480-470-13	Sequence 13, APPL
c	40	9.4	52.2	18	2 US-08-466-397-100	Sequence 100, APPL
c	41	9.4	52.2	18	2 US-08-486-391-100	Sequence 100, APPL
c	42	9.4	52.2	18	2 US-08-461-965-100	Sequence 100, APPL
c	43	9.4	52.2	18	2 US-08-326-110A-13	Sequence 13, APPL
c	44	9.4	52.2	18	2 US-08-634-641-100	Sequence 100, APPL
c	45	9.4	52.2	18	3 US-09-249-471-100	Sequence 100, APPL

RESULT 1
US-08-292-620A-1886
Sequence 1886, Application US/0829620A

PATENT NO. 5837542
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McGuigan
APPLICANT: Sean Sullivan

APPLICANT: Kenneth G. Drayer
TITLE OF INVENTION: RIBONUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATED TO LEVELS OF INTACT CELLULAR ADHESION

TITLE OF INVENTION: RELATED TO LEVELS OF INTACT CELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (1-CAM-1)

NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2" Diskette, 1.44 Mb
COMPILER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1886:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-292-620A-1886

Query Match 63.3%; Score 11.4; DB 2; Length 17;
 Best Local Similarity 92.3%; Pred. No. 7e+02; 1; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCCUAUCGGUUC 16
 Db 2 GGCUGUGGGUGC 14

RESULT 2

US-08-292-620A-1977
 Sequence 1977, Application US/08292620A
 Patent No. 5837542

GENERAL INFORMATION:

APPLICANT: Susan Grimm

APPLICANT: Dan T. Stinchcomb

APPLICANT: James McSwiggen

APPLICANT: Sean Sullivan

APPLICANT: Kenneth G. Draper

TITLE OF INVENTION: RIBOZYME TREATMENT OF

TITLE OF INVENTION: DISEASES OR CONDITIONS

TITLE OF INVENTION: RELATED TO LEVELS OF

TITLE OF INVENTION: INTRACELLULAR ADHESION

TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)

NUMBER OF SEQUENCES: 2390

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2056

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/292,620A

FILING DATE: August 17, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

prior application data: including application

prior application data: described below:

two

COMPUTER READABLE FORM:
 MEDIUM TYPE: 13.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/071,845
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/292,620
 FILING DATE: August 17, 1994
 APPLICATION NUMBER: 08/008,895
 FILING DATE: January 19, 1993
 APPLICATION NUMBER: 07/989,849
 FILING DATE: December 7, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 208/149
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 1886:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-09-071-845-1886

Query Match 63.3%; Score 11.4; DB 3; Length 17;
 Best Local Similarity 92.3%; Pred. No. 7e+02; 1; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCCUAUCGGUUC 16
 Db 2 GGCUGUGGGUGC 14

INFORMATION FOR SEQ ID NO: 1977:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-292-620A-1977

RESULT 4
US-09-071-845-1977
; Sequence 1977 Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; DISEASES OR CONDITIONS
; RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE: January 19, 1993
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1977:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc= "oligonucleotide primer BB-1"
; ANTI-SENSE: YES
; US-08-418-071-6

Query Match 58.9%; Score 10.6; DB 2; Length 20;
Best Local Similarity 58.8%; Pred. No. 2.1e+03; 4; Indels 0; Gaps 0;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
; US-09-071-845-1977

Query Match 58.9%; Score 10.6; DB 2; Length 20;
Best Local Similarity 58.8%; Pred. No. 7e+02; 1; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCCUAUCGGUGC 16
Db 2 GGCGUGCGGUGC 14

RESULT 5
US-08-418-071-6
; Sequence 6, Application US/08418071
; Patent No. 5946705
; GENERAL INFORMATION:

APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
INHIBITING HEPATITIS C
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0

RESULT 6
US-08-182-968A-497/C
; Sequence 497, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
INHIBITING HEPATITIS C
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/182,968A
 FILING DATE: 13-JANUARY-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/882,888

FILING DATE: 14-MAY-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 205/277

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 497:

SEQUENCE CHARACTERISTICS:
 LENGTH: 15
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-474-306A-497
 Query Match 57.8%; Score 10.4; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 2.6e+03; Indels 0; Gaps 0;
 Matches 8; Conservative 3; Mismatches 1;

QY 2 AUGGCCUAUCGG 13
 Db 14 ATGGCCATATTGG 3

RESULT 8

US-09-064-156A-497/C
 Sequence 497, Application US/09064156A
 Patent No. 6133966

GENERAL INFORMATION:
 APPLICANT: Draper, Kenneth G.
 METHOD AND REAGENT FOR
 TITLE OF INVENTION: INHIBITING HEPATITIS C
 TITLE OF INVENTION: VIRUS REPLICATION
 NUMBER OF SEQUENCES: 497
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066

COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/064,156A
 FILING DATE: April 21, 1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/774,306
 FILING DATE: December 26, 1996
 APPLICATION NUMBER: 08/182,968
 FILING DATE: January 13, 1994
 APPLICATION NUMBER: 07/882,888
 FILING DATE: May 14, 1992

PRIOR APPLICATION DATA:
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/774,306A
 FILING DATE: December 26, 1996
 APPLICATION NUMBER: 08/182,968
 FILING DATE: January 13, 1994
 APPLICATION NUMBER: 07/882,888
 FILING DATE: May 14, 1992

ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 224/083
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 497:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-09-064-156A-497
 Query Match 57.8%; Score 10.4; DB 3; Length 15;
 Best Local Similarity 66.7%; Pred. No. 2.6e+03; Indels 0; Gaps 0;
 Matches 8; Conservative 3; Mismatches 1;

QY 2 AUGGCCUAUCGG 13
 Db 14 ATGGCCATATTGG 3

INFORMATION FOR SEQ ID NO: 497:

RESULT 9
US-09-059-779-5
Sequence 5, Application US/09059779

GENERAL INFORMATION:
APPLICANT: Lubert Rubebell Earl A.

APPLICANT: Michael P. Mittmann
TITLE OF INVENTION: Lithographic Mask Design and

NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ritter, Van Pelt & Yi LLP
STREET: 4906 El Camino Real, Suite 205
CITY: Los Altos
STATE: California
COUNTRY: USA

ZIP: 94022
COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenten Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,779
FILING DATE: April 13, 1998

CLASSIFICATION:
NAME: Ritter, Michael J.

REGISTRATION NUMBER: 36,653
REFERENCE/DOCKET NUMBER: AFFY015

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-903-3500

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs

SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/584,040

RESULT 10
US-09-059-779-5
Query Match 56.7%; Score 10.2; DB 3; Length 15;
Best Local Similarity 60.0%; Pred. No. 3.4e+03; Mismatches 3; Indels 0; Gaps 0;
Matches 9; Conservative 3;

Qy	2 AUGGCCUACGGGCG 16	1 : : :	Db	1 ATGGCACATCGATGC 15
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RESULT 11
US-08-584-040-5816
Query Match 56.7%; Score 10.2; DB 4; Length 17;
Best Local Similarity 80.0%; Pred. No. 3.5e+03; Mismatches 3; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 3;

Qy	3 UGGCCUACGGGCG 17	1 1 1	Db	3 UGGCCUACGGGUG 17
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RESULT 11
US-08-584-040-5816
Sequence 5816, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: Storage
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040

FILING DATE: January 11, 1996
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 60/005,974
 FILING DATE: October 26, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 218/064
 TELECOMMUNICATION INFORMATION:
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 5816:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 ; US-08-584-040-5816
 ;
 Query Match 56.7%; Score 10.2; DB 4; Length 17;
 Best Local Similarity 80.0%; Pred. No. 3.5e+03;
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 UGGCCUAUCGGGCG 17
 ||| ||| ||||| |||
 Db 2 UGGCUUUCGGUG 16
 ;
 RESULT 12
 US-08-584-040-5817
 ; Sequence 5817, Application US/08584040
 ; Patent No. 6146398
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Pavco, Pamela
 ; APPLICANT: McSwigan, James
 ; APPLICANT: Escobedo, Jaime
 ; APPLICANT: Stinchcomb, Dan T.
 ;
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 ; TREATMENT OF DISEASES OR
 ; CONDITIONS RELATED TO LEVELS
 ; OF VASCULAR ENDOTHELIAL
 ; TITLE OF INVENTION: TREATMENT OF
 ; TITLE OF INVENTION: OF
 ; TITLE OF INVENTION: GROWTH FACTOR
 ; NUMBER OF SEQUENCES: 8502
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/584,040
 ; FILING DATE: January 11, 1996
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/005,974
 ; FILING DATE: October 26, 1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 218/064
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; US-08-584-040-5817
 ;
 Query Match 56.7%; Score 10.2; DB 4; Length 17;
 Best Local Similarity 80.0%; Pred. No. 3.5e+03;
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 UGGCCUAUCGGGCG 17
 ||| ||| ||||| |||
 Db 1 UGGCUUUCGGUG 15
 ;
 RESULT 13
 US-08-108-837-3
 ; Sequence 3, Application US/09108837
 ; Patent No. 5972617
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: SAMI Manabu
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE FOR DETECTING LACTIC ACID BACTERIA AND
 ; FILE REFERENCE: SAMI1
 ; CURRENT APPLICATION NUMBER: US/09/108, 837
 ; CURRENT FILING DATE: 1998-07-02
 ;
 ; EARLIER APPLICATION NUMBER: 09-195268
 ; EARLIER FILING DATE: 1997-07-07
 ; NUMBER OF SEQ ID NOS: 3
 ; SEQ ID NO 3
 ; LENGTH: 18
 ;
 ; TYPE: DNA
 ; ORGANISM: Lactobacillus brevis
 ; US-09-108-837-3
 ;
 Query Match 56.7%; Score 10.2; DB 2; Length 18;
 Best Local Similarity 60.0%; Pred. No. 3.5e+03;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 AAUGGCCUAUCGGUG 15
 ||| :||| :||| :|:
 Db 1 ATGCCAATCGTGC 15
 ;
 RESULT 14
 US-08-948-097-7
 ; Sequence 7, Application US/08948097C
 ; Patent No. 6103493
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Skerra, Arne
 ; APPLICANT: Voss, Selma
 ; TITLE OF INVENTION: Streptavidin Muteins
 ; FILE REFERENCE: HBR 1119
 ; CURRENT APPLICATION NUMBER: US/08/948,097C
 ; CURRENT FILING DATE: 1997-10-09
 ;
 ; EARLIER APPLICATION NUMBER: DE 196 41 876.3
 ; EARLIER FILING DATE: 1996-10-10
 ; NUMBER OF SEQ ID NOS: 17
 ; SEQ ID NO 7
 ; LENGTH: 12
 ;
 ; TYPE: DNA
 ;
 ; ORGANISM: Artificial sequence
 ; FEATURE: CDS
 ; NAME/KEY: CDS
 ; OTHER INFORMATION: Synthesized
 ; US-08-948-097-7
 ;
 Query Match 55.6%; Score 10; DB 3; Length 12;
 Best Local Similarity 80.0%; Pred. No. 4.4e+03;

Matches	8;	Conservative	2;	Mismatches	0;	Indels	0;	Gaps	0;
Oy	9	AUCGGUGCGGA 18							
	:								
Db	1	ATCGGTCGGA 10							

RESULT 15
US-08-222-17A-108/c

; Sequence 108, Application US/0822217A

; Patent No. 5,829,79

; GENERAL INFORMATION:

APPLICANT: Weber, James L.

TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
NUMBER OF SEQUENCES: (dC-dA)n (dG-dT)n SEQUENCES AND METHODS OF USING SAME
CORRESPONDENCE ADDRESS:

ADDRESSEE: Dewitt Ross & Stevens, S.C.
CITY: Madison
STREET: 8000 EXCELSIOR Drive, Suite 401
STATE: Wisconsin
COUNTRY: USA
ZIP: 53717-1914

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/222,17A
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989

ATTORNEY/AGENT INFORMATION:

NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
TELEX:

INFORMATION FOR SEQ ID NO: 108:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: mtdnaapl

US-08-222-17A-108

Query Match 55.6%; Score 10; DB 1; Length 20;
Best Local Similarity 61.1%; Pred. No. 4.7e+03; Indels 5;
Matches 11; Conservative 2; Mismatches 0; Gaps 0;

Qy	1	AAUGGCCUAUCCGGCGGA 18
	: :	
Db	18	ATGGCCCAAGGGTmAGA 1

Search completed: May 22, 2003, 20:18:25
Job time : 40.7273 secs

GenCore version 5.1.4_p5-4578
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Om nucleic - nucleic search, using sw model

Run on:

May 22, 2003, 19:36:48 ; Search time 85.0309 seconds

(without alignments) updates/sec
279.329 Million cell

title: US-09-780-929-98

Perfect score: 18

Sequence: aauggcuaucggugcga 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters:

191488

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_NA: *

1: /cgpn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq: *

2: /cgpn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq: *

3: /cgpn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq: *

4: /cgpn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq: *

5: /cgpn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq: *

6: /cgpn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq: *

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11: /cgpn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq: *

12: /cgpn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq: *

13: /cgpn2_6/ptodata/1/pubpna/US10_NEW_PUBCOMB.seq: *

14: /cgpn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

No. Score Query Match Length DB ID Description

1 18 100.0 19 10 US-09-780-929-98 Sequence 98, Appl

2 11.2 62.2 17 9 US-09-780-533A-633 Sequence 633, Appl

3 11.2 62.2 19 9 US-09-796-081-3 Sequence 3, Appl

4 10.4 57.8 15 10 US-09-504-231A-519 Sequence 4, Appl

5 10.4 57.8 15 10 US-09-274-530A-519 Sequence 519, Appl

6 10.4 57.8 18 10 US-09-969-373-3464 Sequence 516, Appl

7 10.4 57.8 20 9 US-10-068-160-36 Sequence 36, Appl

8 10.2 56.7 17 9 US-09-780-533A-2300 Sequence 2300, Appl

9 10.2 56.7 18 9 US-09-961-700A-29 Sequence 2612, Appl

10 10.2 55.6 20 9 US-09-232-785-373 Sequence 29, Appl

11 10.2 55.6 17 9 US-09-825-805-373 Sequence 737, Appl

12 10.2 55.6 18 9 US-09-960-373-2070 Sequence 29, Appl

13 10.2 55.6 17 9 US-09-961-700A-29 Sequence 373, Appl

14 9.8 54.4 17 9 US-09-822-805-373 Sequence 712, Appl

15 9.6 53.3 17 9 US-09-961-077-264 Sequence 264, Appl

16 9.6 53.3 17 9 US-09-848-754A-1942 Sequence 1942, Appl

17 9.6 53.3 17 9 US-09-848-754A-3017 Sequence 3017, Appl

18 9.6 53.3 18 9 US-09-961-077-643 Sequence 643, Appl

ALIGNMENTS

RESULT 1

US-09-780-929-98

Sequence 98, Application US/09780929

Patent No: US20020151693A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc

APPLICANT: Breaker, Ronald

APPLICANT: Bergelman, Leo

FILE REFERENCE: MBH00-884-H (500-001)

CURRENT APPLICATION NUMBER: US/09-780,929

CURRENT FILING DATE: 2001-07-08

PRIORITY APPLICATION NUMBER: US 60/181,360

PRIORITY FILING DATE: 2000-02-08

NUMBER OF SEQ ID NOS: 126

SOFTWARE: PatentIn version 3.0

SEQ ID NO 98

LENGTH: 18

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence:

US-09-780-929-98

Query Match 100.0%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.87%;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Qy 1 AUGGCCUAUCGGUGCGA 18
Dy 1 AAUGGCCUAUCGGUGCGA 18

RESULT 2

Publication No. US20030060611A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Blatt, Larry

APPLICANT: McSwigan, Jim

APPLICANT: Chowria, Bharat

APPLICANT: Haeblerli, Pete
 TITLE OF INVENTION: Method and Reagent for the Inhibition of Nogo Gene
 FILE REFERENCE: MBH00-878-A (400/011)
 CURRENT APPLICATION NUMBER: US/09/780,533A
 CURRENT FILING DATE: 2001-02-09
 PRIORITY APPLICATION NUMBER: US 60/181,797
 PRIORITY FILING DATE: 2000-02-11
 NUMBER OF SEQ ID NOS: 6679
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 633
 LENGTH: 17
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-09-780-533A-633

Query Match 62.2%; Score 11.2; DB 9; Length 17;
 Best Local Similarity 56.2%; Pred. No. 5.9e+03; Mismatches 3; Indels 0; Gaps 0;
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAUGGCCUAUAGGGUC 16
 ||:|| |:||:| :|||
 Db 16 ATGATCTATCTGTGC 1

RESULT 3
 US-09-796-081-3
 Sequence 3, Application US/09796081
 Publication No. US20030045538A1
 GENERAL INFORMATION:
 APPLICANT: Danaboyina, Ramaiah
 APPLICANT: Nadukkudy, Varghese E.
 APPLICANT: Joshy, Joseph
 TITLE OF INVENTION: VIOLGEN LINKED ACRIDINE BASED MOLECULE AND PROCESS FOR
 TITLE OF INVENTION: THE PREPARATION THEREOF
 FILE REFERENCE: 3108/10342
 CURRENT APPLICATION NUMBER: US/09/796,081
 CURRENT FILING DATE: 2001-08-14
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3
 LENGTH: 19
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: synthetic oligonucleotide
 US-09-796-081-3

Query Match 62.2%; Score 11.2; DB 9; Length 19;
 Best Local Similarity 56.2%; Pred. No. 5.9e+03; Mismatches 3; Indels 0; Gaps 0;
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAUGGCCUAUAGGGUC 16
 ||:|| |:||:| :|||
 Db 2 ACTGGCCTTTCGGTGC 17

RESULT 4
 US-09-796-081-4/C
 Sequence 4, Application US/09796081
 Publication No. US20030045538A1
 GENERAL INFORMATION:
 APPLICANT: Danaboyina, Ramaiah
 APPLICANT: Nadukkudy, Varghese E.
 APPLICANT: Joshy, Joseph
 TITLE OF INVENTION: VIOLGEN LINKED ACRIDINE BASED MOLECULE AND PROCESS FOR
 TITLE OF INVENTION: THE PREPARATION THEREOF
 FILE REFERENCE: 3108/01342
 CURRENT APPLICATION NUMBER: US/09/796,081
 CURRENT FILING DATE: 2001-08-14
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 4
 LENGTH: 19

RESULT 5
 US-09-504-231A-519/C
 Sequence 519, Application US/09504231A
 Publication No. US20020013458A1
 GENERAL INFORMATION:
 APPLICANT: Blatt, Lawrence
 APPLICANT: McSwiggen, James
 APPLICANT: Roberts, Beth
 APPLICANT: Pavco, Pamela
 APPLICANT: Macelak, Dennis
 TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS REL
 TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
 FILE REFERENCE: IPI 247/282
 CURRENT FILING DATE: 2000-02-15
 PRIORITY APPLICATION NUMBER: 09/274,553
 PRIORITY FILING DATE: 1999-03-23
 PRIORITY APPLICATION NUMBER: 09/257,608
 PRIORITY FILING DATE: 1999-02-24
 PRIORITY APPLICATION NUMBER: 60/100,842
 PRIORITY FILING DATE: 1998-09-18
 PRIORITY APPLICATION NUMBER: 60/083,217
 PRIORITY FILING DATE: 1998-04-27
 NUMBER OF SEQ ID NOS: 3242
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 519
 LENGTH: 15
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
 US-09-504-231A-519

Query Match 57.8%; Score 10.4; DB 10; Length 15;
 Best Local Similarity 66.7%; Pred. No. 1.7e+04; Mismatches 1; Indels 0; Gaps 0;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 AUGGCCUAUAGGG 13
 ||:|||:|| :|||
 Db 14 ATGGCCTATGG 3

RESULT 6
 US-09-274-553D-519/C
 Sequence 519, Application US/09274553D
 Publication No. US20020082225A1
 GENERAL INFORMATION:
 APPLICANT: Blatt, Lawrence
 APPLICANT: McSwiggen, James
 APPLICANT: Roberts, Beth
 APPLICANT: Pavco, Pamela
 APPLICANT: Macelak, Dennis
 TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS REL
 TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
 FILE REFERENCE: IPI 247/282
 CURRENT APPLICATION NUMBER: US/09/274,553D
 CURRENT FILING DATE: 1999-03-23
 PRIORITY APPLICATION NUMBER: 60/257,608

PRIOR FILING DATE: 1999-02-24
 PRIOR APPLICATION NUMBER: 60/100,842
 PRIORITY FILING DATE: 1998-09-18
 PRIOR APPLICATION NUMBER: 60/083,217
 NUMBER OF SEQ ID NOS: 3148
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 519
 LENGTH: 15
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid target
 US-09-274-553D-519

QY	2 AUGGCCUAUCGG 13	5 GCCUAUCCGGUGC 16
Db	: : : 14 ATGGCTTATGG 3	: : 15 GCCTATCCGATGC 4

Query Match 57.8%; Score 10.4; DB 10; length 15;
 Best Local Similarity 66.7%; Pred. No. 1.7e+04;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

RESULT 7
 US-09-969-373-3464/c
 Sequence 3464 Application US/09969373
 Patent No. US20020133852A1
 GENERAL INFORMATION:
 APPLICANT: Effertz, Roger J.
 APPLICANT: Hauge, Brian M.
 TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
 FILE REFERENCE: 38-10(52679)A
 CURRENT APPLICATION NUMBER: US/09/969, 373
 CURRENT FILING DATE: 2001-10-02
 PRIOR APPLICATION NUMBER: US 09/7754, 853
 PRIOR FILING DATE: 2001-01-05
 PRIOR APPLICATION NUMBER: US 09/7760, 427
 PRIOR FILING DATE: 2001-01-13
 PRIOR APPLICATION NUMBER: US 09/855, 768
 PRIOR FILING DATE: 2001-05-15
 NUMBER OF SEQ ID NOS: 4593
 SEQ ID NO 3464
 LENGTH: 18
 TYPE: DNA
 ORGANISM: Glycine max
 US-09-969-373-3464

Query Match 57.8%; Score 10.4; DB 10; length 18;
 Best Local Similarity 66.7%; Pred. No. 1.7e+04;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

RESULT 8
 US-10-058-160-36/c
 Sequence 36 Application US/10068160
 Publication No. US2003006040A1
 GENERAL INFORMATION:
 APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
 APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
 APPLICANT: KLINMAN, Dennis
 APPLICANT: ISHII, Ken
 APPLICANT: VERTHEIL, Daniela
 TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
 FILE REFERENCE: 4239-61999
 CURRENT APPLICATION NUMBER: US/10/068, 160
 CURRENT FILING DATE: 2002-02-06
 PRIOR APPLICATION NUMBER: 60/128, 898
 PRIOR FILING DATE: 1999-04-12

Query Match 57.8%; Score 10.4; DB 9; Length 20;
 Best Local Similarity 66.7%; Pred. No. 1.7e+04;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

RESULT 9
 US-09-780-533A-2300/c
 Sequence 2300 Application US/09780533A
 Publication No. US2003006061A1
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Blatt, Larry
 APPLICANT: McSwiggen, Jim
 APPLICANT: Chowkira, Bharat
 APPLICANT: Haerterl, Pete
 TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
 FILE REFERENCE: MBHB00/878-A (400/011)
 CURRENT APPLICATION NUMBER: US/09/780,533A
 CURRENT FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: US 60/181,797
 NUMBER OF SEQ ID NOS: 6679
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 2300
 LENGTH: 17
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-09-780-533A-2300

Query Match 56.7%; Score 10.2; DB 9; Length 17;
 Best Local Similarity 53.3%; Pred. No. 2.2e+04;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

RESULT 10
 US-09-780-533A-2662/c
 Sequence 2662 Application US/09780533A
 Publication No. US2003006061A1
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Blatt, Larry
 APPLICANT: McSwiggen, Jim
 APPLICANT: Chowkira, Bharat
 APPLICANT: Haerterl, Pete
 TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
 FILE REFERENCE: MBHB00/878-A (400/011)
 CURRENT APPLICATION NUMBER: US/09/780,533A
 CURRENT FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: US 60/181,797
 PRIOR FILING DATE: 2000-02-11
 NUMBER OF SEQ ID NOS: 6679
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 2662
 LENGTH: 17
 TYPE: RNA

; ORGANISM: Homo sapiens
 US-09-780-929-98.szlm20.rnpb

Query Match ; Score 56.7%; Pred. No. 2.2e+04; Length 17;
 Best Local Similarity 53.3%; Pred. No. 2.2e+04;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAUGGCCUAUCGGUG 15
 ||:|| |:|:|| |:
 Db 15 AATGATCTATCTG 1

RESULT 11
 US-09-969-373-2070
 ; Sequence 2070, Application US/09969373
 ; Patent No. US20020133852A1
 ; GENERAL INFORMATION:
 APPLICANT: Haage, Brian M.
 TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
 FILE REFERENCE: 38-10526791A
 CURRENT APPLICATION NUMBER: US/09/969,373
 CURRENT FILING DATE: 2001-10-02
 PRIOR APPLICATION NUMBER: US 09/7754,853
 PRIOR FILING DATE: 2001-01-05
 PRIOR APPLICATION NUMBER: US 09/7760,427
 PRIOR FILING DATE: 2001-01-13
 PRIOR APPLICATION NUMBER: US 09/855,768
 PRIOR FILING DATE: 2001-05-15
 NUMBER OF SEQ ID NOS: 4593
 SEQ ID NO 2070
 LENGTH: 18
 TYPE: DNA
 ORGANISM: Glycine max
 US-09-969-373-2070

Query Match ; Score 56.7%; Pred. No. 2.2e+04; Length 18;
 Best Local Similarity 60.0%; Pred. No. 2.2e+04;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAUGGCCUAUCGGUG 15
 ||:||:|| |:|:
 Db 4 AATGCCAATTGCTG 18

RESULT 12
 US-09-961-700A-29
 ; Sequence 29, Application US/09961700A
 ; Publication No. US20020187482A1
 ; GENERAL INFORMATION:
 APPLICANT: Liang, Zicai
 APPLICANT: Zhang, Hong-Yan
 APPLICANT: Wahlestedt, Claes
 TITLE OF INVENTION: Methods and Means of RNA Analysis
 FILE REFERENCE: 13522-003001
 CURRENT APPLICATION NUMBER: US/09/961,700A
 CURRENT FILING DATE: 2002-07-23
 PRIOR APPLICATION NUMBER: 60/235,029
 PRIOR FILING DATE: 2001-09-25
 NUMBER OF SEQ ID NOS: 71
 SEQ ID NO 29
 LENGTH: 18
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Synthetically generated oligonucleotide
 US-09-961-700A-29

Query Match ; Score 55.6%; Pred. No. 2.8e+04; Length 18;
 Best Local Similarity 50.0%; Pred. No. 2.8e+04;
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 AAUGGCCUAUCGGUGCGGA 18
 ||:|| |:| :|| |:
 Db 1 AATGGGCTTCTGTCGTGA 18

RESULT 13
 US-09-232-785-373/C
 ; Sequence 373, Application US/09232785
 ; Publication No. US20030049612A1
 ; GENERAL INFORMATION:
 APPLICANT: International Paper Co.
 APPLICANT: Echt, Craig S.
 APPLICANT: Nelson, C. Dana
 TITLE OF INVENTION: MICROSATELITE DNA MARKERS AND USES
 FILE REFERENCE: 481/1E188US1
 CURRENT APPLICATION NUMBER: US/09/232,785
 CURRENT FILING DATE: 1999-01-19
 PRIOR APPLICATION NUMBER: 09/232,884
 PRIOR FILING DATE: 1999-01-15
 NUMBER OF SEQ ID NOS: 397
 SOFTWARE: PastSeq for Windows Version 3.0
 SEQ ID NO 373
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Pinus taeda L.
 US-09-232-785-373

Query Match ; Score 55.6%; Pred. No. 2.8e+04; Length 20;
 Best Local Similarity 55.6%; Pred. No. 2.8e+04;
 Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 AAUGGCCUAUCGGUGCGGA 18
 ||:|| |:| :|| |:
 Db 18 AATGGCTTCTGCGGACCA 1

RESULT 14
 US-09-828-805-737
 ; Sequence 737, Application US/09825805
 ; Publication No. US20030004122A1
 ; GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Beigelman, Leo
 APPLICANT: Beaudry, Amber
 APPLICANT: Karpeisky, Alex
 APPLICANT: Adamic, Jasenka Matulic
 APPLICANT: Sweeney, Shawn
 APPLICANT: Zinner, Dave
 TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleotides
 FILE REFERENCE: MBHB00-831-F (400/009)
 CURRENT APPLICATION NUMBER: US/09/825,805
 CURRENT FILING DATE: 2001-09-27
 PRIOR APPLICATION NUMBER: 09/5378,223
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 09/476,387
 PRIOR FILING DATE: 1999-12-30
 PRIOR APPLICATION NUMBER: 09/474,432
 PRIOR FILING DATE: 1999-12-29
 PRIOR APPLICATION NUMBER: 09/301,511
 PRIOR FILING DATE: 1999-04-28
 PRIOR APPLICATION NUMBER: 09/186,675
 PRIOR FILING DATE: 1998-11-04
 PRIOR APPLICATION NUMBER: 60/083,727
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/064,866
 PRIOR FILING DATE: 1997-11-05
 NUMBER OF SEQ ID NOS: 1558
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 737
 LENGTH: 17
 TYPE: RNA
 ORGANISM: Homo sapiens

US-09-825-805-717

Query Match 54.4%; Score 9.8; DB 9; Length 17;
 Best Local Similarity 84.6%; Pred. No. 3.6e+04;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCUAUUCGGGUGCGA 18
 Db 5 CCUACGGGAGCGA 17

RESULT 15

US-09-825-805-712

Sequence 712, Application US/09825805
 Publication No. US20030004122A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Beigelman, Leo

APPLICANT: Beaudry, Amber

APPLICANT: Karpeisky, Alex

APPLICANT: Adamic, Jasenka Matulic

APPLICANT: Zinnen, Shawn

APPLICANT: Swedler, Dave

APPLICANT: Zinnen, Shawn

TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleotides

FILE REFERENCE: MBHB00-831-F (400/009)

CURRENT APPLICATION NUMBER: US/09/825,805

CURRENT FILING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: 09/578,223

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 09/476,387

PRIOR FILING DATE: 1999-12-30

PRIOR APPLICATION NUMBER: 09/474,432

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: 09/301,511

PRIOR FILING DATE: 1999-04-28

PRIOR APPLICATION NUMBER: 09/186,675

PRIOR FILING DATE: 1998-11-04

PRIOR APPLICATION NUMBER: 60/083,727

PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/064,866

PRIOR FILING DATE: 1997-11-05

NUMBER OF SEQ ID NOS: 1558

SOFTWARE: PatentIn version 3.0

SEQ ID NO 712

LENGTH: 17

TYPE: RNA

ORGANISM: Homo sapiens

US-09-825-805-712

Query Match 53.3%; Score 9.6; DB 9; Length 17;
 Best Local Similarity 75.0%; Pred. No. 4.7e+04;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 UGGCCUAUCGGGUGCGA 18
 Db 2 UGCCCAUCGGGUGCGA 17

Search completed: May 22, 2003, 21:38:48
 Job time : 87.099 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

Om nucleic - nucleic search, using sw model

Run on:

May 22, 2003, 18:59:38 ; Search time 2074.36 seconds

(without alignments) 218.170 Million cell updates/sec

Title: US-09-780-929-98

Perfect score: 18

Sequence: IDENTITY_NUC

Scoring table: Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

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2: /cgn2_6/ptodata/1/pna/us06_COMB.seq:*

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5: /cgn2_6/ptodata/1/pna/us081_COMB.seq:*

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9: /cgn2_6/ptodata/1/pna/us05_COMB.seq:*

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11: /cgn2_6/ptodata/1/pna/us087_COMB.seq:*

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31: /cgn2_6/ptodata/1/pna/us098A_COMB.seq:*

32: /cgn2_6/ptodata/1/pna/us098B_COMB.seq:*

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41: /cgn2_6/ptodata/1/pna/us101B_COMB.seq:*

42: /cgn2_6/ptodata/1/pna/us102A_COMB.seq:*

43: /cgn2_6/ptodata/1/pna/us102B_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2	18	100.0	18	US-09-780-929-98 Sequence 98, Appl
c	c	12.2	30	31	US-09-837-383-803 Sequence 650, Appl
c	c	67.8	20	31	US-09-837-383-803 Sequence 650, Appl
c	3	12.2	67.8	20	US-09-837-383-803 Sequence 650, Appl
c	4	12.2	67.8	20	US-09-837-383-803 Sequence 650, Appl
c	5	12.2	67.8	20	US-09-837-383-803 Sequence 650, Appl
c	6	12.2	67.8	20	US-09-837-383-803 Sequence 650, Appl
c	7	11.8	65.6	1	PCT-US02-25943-18265 Sequence 18265, A
c	8	11.8	65.6	16	PCT-US02-25943-18265 Sequence 18265, A
c	9	11.8	65.6	16	PCT-US02-25943-18265 Sequence 18265, A
c	10	11.8	65.6	16	PCT-US02-25943-18265 Sequence 18265, A
c	11	11.4	63.3	20	US-09-198-452A-3336 Sequence 3336, Ap
c	12	11.4	63.3	20	US-09-198-452A-3336 Sequence 3336, Ap
c	13	11.4	63.3	20	US-09-198-452A-3336 Sequence 3336, Ap
c	14	11.2	62.2	17	US-09-198-452A-3336 Sequence 3336, Ap
c	15	11.2	62.2	17	US-09-198-452A-3336 Sequence 3336, Ap
c	16	11.2	62.2	19	US-09-198-452A-3336 Sequence 3336, Ap
c	17	11.2	62.2	19	US-09-198-452A-3336 Sequence 3336, Ap
c	18	11.2	62.2	20	US-09-198-452A-3336 Sequence 3336, Ap
c	19	10.8	60.0	15	PCT-US02-25940-18232 Sequence 16232, A
c	20	10.8	60.0	15	PCT-US02-25940-18232 Sequence 16232, A
c	21	10.8	60.0	15	PCT-US02-25942-1512 Sequence 1512, Ap


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; LOCATION: (1820695)..(1820710)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 19657
US-10-227-565-18265

Query Match Similarity 65.6%; Score 11.8; DB 42; Length 16;
Best Local Similarity 73.3%; Pred. No. 3.3e+04; DB 42; Length 16;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 4 GACCUAUCGGUGCGA 18
Db 2 GGCTTATGCCGCCGA 16

RESULT 10
US-09-198-452A-3336/c
Sequence 3336, Application US/09198452A
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments, and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 3336
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-3336
Query Match Similarity 65.6%; Score 11.8; DB 15; Length 20;
Best Local Similarity 66.7%; Pred. No. 3.5e+04; DB 15; Length 20;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AATGCCUAUCGUG 15
Db 20 AATGCCTAACGATG 6

RESULT 11
US-09-703-708-17627
Sequence 17627, Application US/09703708
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley G.
; APPPLICANT: Hinkle, Gregory J.
; TITLE OF INVENTION: Xanthomonas campestris Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10/15804/C
; CURRENT APPLICATION NUMBER: US/09/183,791
; CURRENT FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 18992
; SEQ ID NO 17627
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Xanthomonas campestris
US-09-703-708-17627

Query Match Similarity 65.3%; Score 11.4; DB 60; Length 20;
Best Local Similarity 66.5%; Pred. No. 6e+04; DB 60; Length 20;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 3 UGGCCUAUCGUG 15
Db 2 TGGCTTATCGTG 14

RESULT 13
US-60-183-791-17627
Sequence 17627, Application US/60183791
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley G.
; APPPLICANT: Hinkle, Gregory J.
; TITLE OF INVENTION: Xanthomonas campestris Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10/15804/B
; CURRENT APPLICATION NUMBER: US/60/183,791
; CURRENT FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 18992
; SEQ ID NO 17627
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Xanthomonas campestris
US-60-183-791-17627

Query Match Similarity 63.3%; Score 11.4; DB 62; Length 20;
Best Local Similarity 61.5%; Pred. No. 6e+04; DB 62; Length 20;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 3 UGGCCUAUCGUG 15
Db 2 TGGCTTATCGTG 14

RESULT 14
US-09-546-745A-1992/c
Sequence 1992, Application US/09546745A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: Zwick, Michael
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules
; FILE REFERENCE: 237/133
; CURRENT APPLICATION NUMBER: US/09/546,745A
; CURRENT FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 7043
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1992
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-546-745A-1992

Query Match Similarity 63.3%; Score 11.4; DB 28; Length 20;
Best Local Similarity 61.5%; Pred. No. 6e+04; DB 28; Length 20;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 3 UGGCCUAUCGUG 15
Db 2 TGGCTTATCGTG 14

RESULT 12
US-60-164-320-17627
Sequence 17627, Application US/60164320

Query Match Similarity 62.2%; Score 11.2; DB 21; Length 17;

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Best Local Similarity 62.5%; Pred. No. 7.8e+04; Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
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 Db 16 TGGCCCATAGGTGCCA 1

RESULT 15
 US-09-780-533A-633/c
 Sequence 633, Application US/09780533A
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Blatt, Larry
 APPLICANT: McSwiggen, Jim
 APPLICANT: Chowdhury, Bharat
 APPLICANT: Haeberli, Pete
 TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
 FILE REFERENCE: MBHB00-878-A (40/011)
 CURRENT APPLICATION NUMBER: US/09/780,533A
 CURRENT FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: US 60/181,797
 PRIOR FILING DATE: 2000-02-11
 NUMBER OF SEQ ID NOS: 6679
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 633
 LENGTH: 17
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-09-780-533A-633

Query Match 62.2%; Score 11.2; DB 30; Length 17;
 Best Local Similarity 56.2%; Pred. No. 7.8e+04;
 Matches 9; Conservative 4; Mismatches 3;
 Indels 0; Gaps 0;

Qy 1 AAUGGCCUAUGGGUGC 16
 Db 16 AATGATCTATCTGTC 1

Search completed: May 22, 2003, 21:22:05
 Job time : 2076.36 secs

GenCore version 5.1.4_p5 4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 19:04:38 ; Search time 445.636 Seconds

(without alignments) updates/sec 209.509 Million cell

Title: US-09-780-929-98

Perfect score: 18

Sequence: 1 aauggccauacggcgca 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6438716 seqs, 2593167500 residues

Total number of hits satisfying chosen parameters:

667140

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-Processing: Maximum Match 0%

Listing first 45 summaries

Database : Pending_Patents_NA_New:*

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4: /cgn2_6/podata/2/pna/US8_NEU_COMBO.seq:*
5: /cgn2_6/podata/2/pna/US9_NEU_COMBO.seq:*
6: /cgn2_6/podata/2/pna/US9_NEU_COMBO.seq2:*
7: /cgn2_6/podata/2/pna/US9_NEU_COMBO.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result

No. Score Query Match Length DB IDO

Description

ALIGNMENTS

C	23	10.4	57.8	16	8	US-10-287-787-20529	Sequence 20529, A
C	24	10.4	57.8	16	8	US-10-287-787-26977	Sequence 26977, A
C	25	10.4	57.8	17	9	US-10-084-839-3310	Sequence 3310, A
C	26	10.4	57.8	18	8	US-10-299-054A-7571	Sequence 7571, A
C	27	10.4	57.8	18	8	US-10-299-054A-11547	Sequence 11547, A
C	28	10.4	57.8	19	9	US-10-259-275-73	Sequence 73, A
C	29	10.4	57.8	19	9	PCT-US02-40955-22	Sequence 4, Appl
C	30	10.4	57.8	20	1	US-10-274-586-88	Sequence 22, Appl
C	31	10.4	57.8	20	8	US-10-367-892-10363	Sequence 88, Appl
C	32	10.2	56.7	15	8	US-10-367-892-12851	Sequence 10363, A
C	33	10.2	56.7	15	8	US-10-367-892-14893	Sequence 12851, A
C	34	10.2	56.7	15	8	US-10-367-892-22461	Sequence 22461, A
C	35	10.2	56.7	15	8	US-10-287-787-1285	Sequence 1285, AP
C	36	10.2	56.7	15	8	US-10-287-787-1488	Sequence 1488, AP
C	37	10.2	56.7	15	8	US-10-287-787-6615	Sequence 6615, AP
C	38	10.2	56.7	15	8	US-10-287-787-6616	Sequence 6616, AP
C	39	10.2	56.7	15	8	US-10-287-787-1939	Sequence 19393, A
C	40	10.2	56.7	15	8	US-10-287-787-1939	Sequence 6101, AP
C	41	10.2	56.7	16	8	US-10-367-892-6101	Sequence 6102, AP
C	42	10.2	56.7	16	8	US-10-367-892-6102	Sequence 4121, AP
C	43	10.2	56.7	16	8	US-10-299-054A-4121	Sequence 5693, AP
C	44	10.2	56.7	16	8	US-10-299-054A-5693	
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Query Match	65.6%	Score 11.8;	DB 1;	Length 19;	Sequence 20529, A
Best Local Similarity	86.7%	Pred. No.	8.1e+03;	Indels 0;	Sequence 26977, A
Matches	13;	Conservative	0;	Mismatches 2;	Sequence 3310, A
Other Information:	Description of Artificial Sequence:	Target sequence/siNA sens			Sequence 7571, A
PCT-US03-04088-255					Sequence 11547, A

Qry	3	UGGCCUAUCGGGCG	17		
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Db 5 UGGCCANUCCGUGCG 19

; CURRENT FILING DATE: 2003-01-13

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LOCATION: (2409107)..(2409121) ; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 23195
 US-10-367-892-19783

Query Match ; Sequence 1079, Application US/10303778
 Best Local Similarity 60.0%; Score 10.8; DB 8; Length 15;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 SEQ ID NO: 23057 LENGTH: 16

APPLICANT: RosettaGenomics

GENERAL INFORMATION:

TITLE OF INVENTION: BIINFORMATIICALLY DETECTABLE GROUP OF NOVEL VIRAL TITLE REFERENCE: 47416 CURRENT APPLICATION NUMBER: US/10/303,778 CURRENT FILING DATE: 2002-11-25 NUMBER OF SEQ ID NOS: 17608 SOFTWARE: Patentin version 3.1

SEQ ID NO: 1079 LENGTH: 15

TYPE: DNA ORGANISM: Homo sapiens

US-10-303-778-1079

Query Match ; Sequence 33, Application PC/TU03/10154
 Best Local Similarity 64.3%; Score 10.8; DB 9; Length 15;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

APPLICANT: XOMA TECHNOLOGY LTD.

GENERAL INFORMATION:

TITLE OF INVENTION: Methods and Materials For Increasing Expression of Recombinant FILE REFERENCE: 13698W01 CURRENT APPLICATION NUMBER: PC/TU03/10154 CURRENT FILING DATE: 2003-03-31 PRIORITY APPLICATION NUMBER: US 60/368,530 PRIOR FILING DATE: 2002-03-29 NUMBER OF SEQ ID NOS: 79 SOFTWARE: Patentin version 3.2

SEQ ID NO: 33 LENGTH: 17

TYPE: DNA ORGANISM: Homosapiens

FEATURE: NAME/KEY: misc-feature OTHER INFORMATION: ING-1 Heavy Chain Oligos Low Risk Primers -Reverse Primer GR FEATURE: NAME/KEY: misc-feature OTHER INFORMATION: ING-1 Heavy Chain Oligos Low Risk Primers Reverse Primer GR

PCT US03/10154-33

Query Match ; Sequence 33, Application US/10404724
 Best Local Similarity 71.4%; Score 10.8; DB 1; Length 17;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

APPLICANT: Horwitz, Arnold H.

GENERAL INFORMATION:

TITLE OF INVENTION: Methods and Materials For Increasing Expression of Recombinant FILE REFERENCE: 13698US01 CURRENT APPLICATION NUMBER: US/10/404,724 CURRENT FILING DATE: 2003-03-31 PRIORITY APPLICATION NUMBER: US 60/368,530 PRIOR FILING DATE: 2002-03-29 NUMBER OF SEQ ID NOS: 79

RESULT 7 ; Sequence 1079, Application US/10303778
 General Information:
 Applicant: RosettaGenomics
 Title of Invention: BIINFORMATIICALLY DETECTABLE GROUP OF NOVEL VIRAL
 File Reference: 47416
 Current Application Number: US/10/303,778
 Current Filing Date: 2002-11-25
 Number of Seq Id Nos: 17608
 Software: Patentin version 3.1
 Seq Id No: 1079
 Length: 15
 Type: DNA
 Organism: Homo sapiens

RESULT 8 ; Sequence 23056, Application US/10287787
 General Information:
 Applicant: Feldmann, Richard J.; Global Determinants, Inc.
 Title of Invention: Caulobacter crescentus complete genome.
 File Reference: Jim Zeger Law Offices - 703-684-8333
 Current Application Number: US/10/287,787
 Current Filing Date: 2003-03-03
 Number of Seq Id Nos: 27958
 Software: Proprietary
 Seq Id No: 23056
 Length: 16
 Type: DNA
 Organism: Caulobacter crescentus complete genome.

RESULT 9 ; Sequence 23057, Application US/10287787
 General Information:
 Applicant: Feldmann, Richard J.; Global Determinants, Inc.
 Title of Invention: Chromosome = 1 Strand = negative ConnectronObjectNumber = 25456
 File Reference: 47416
 Current Application Number: US/10/303,778
 Current Filing Date: 2002-11-25
 Number of Seq Id Nos: 79

RESULT 10 ; Sequence 33, Application PC/TU03/10154
 General Information:
 Applicant: XOMA TECHNOLOGY LTD.

General Information:
 Title of Invention: Methods and Materials For Increasing Expression of Recombinant
 File Reference: 13698W01
 Current Application Number: PC/TU03/10154
 Current Filing Date: 2003-03-31
 Priority Application Number: US 60/368,530
 Prior Filing Date: 2002-03-29
 Number of Seq Id Nos: 79
 Software: Patentin version 3.2
 Seq Id No: 33
 Length: 17
 Type: DNA
 Organism: Homosapiens
 Feature: Name/Key: misc-feature
 Other Information: ING-1 Heavy Chain Oligos Low Risk Primers -Reverse Primer GR
 Feature: Name/Key: misc-feature
 Other Information: ING-1 Heavy Chain Oligos Low Risk Primers Reverse Primer GR

PCT US03/10154-33

Query Match ; Sequence 33, Application US/10404724
 Best Local Similarity 71.4%; Score 10.8; DB 1; Length 17;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

APPLICANT: Horwitz, Arnold H.

GENERAL INFORMATION:

TITLE OF INVENTION: Methods and Materials For Increasing Expression of Recombinant FILE REFERENCE: 13698US01 CURRENT APPLICATION NUMBER: US/10/404,724 CURRENT FILING DATE: 2003-03-31 PRIORITY APPLICATION NUMBER: US 60/368,530 PRIOR FILING DATE: 2002-03-29 NUMBER OF SEQ ID NOS: 79

SOFTWARE: PatentIn version 3.2 ;
SEQ ID NO 33 ;
LENGTH: 17 ;
TYPE: DNA ;
ORGANISM: HomoSapiens
FEATURE: NAME/KEY: misc_feature ;
OTHER INFORMATION: ING-1 Heavy Chain Oligos Low Risk Primers -Reverse Primer GR
FEATURE: NAME/KEY: misc_feature ;
OTHER INFORMATION: ING-1 Heavy Chain Oligos Low Risk Primers Reverse Primer GR
US-10-404-724-33
Query Match 60.0%; Score 10.8; DB 8; Length 17;
Best Local Similarity 71.4%; Pred. No. 3e+04;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AAUGGCCUAUCGGU 14
Db 15 AAGGGCCCATCGGT 2

RESULT 12
US-10-237-016A-39/c
Sequence 39, Application US/10237016A
GENERAL INFORMATION:
APPLICANT: OHSUBO, KENICHI
APPLICANT: OKADOME, HIROSHI
APPLICANT: NAKAMURA, SUMIKO
APPLICANT: HARAGUCHI, KAZUTOMO
APPLICANT: YOZA, KOUTICHI
APPLICANT: OKUNISHI, TOMOYA
APPLICANT: SUZUKI, KEITARO
TITLE OF INVENTION: DNA-LEVEL RICE PALATABILITY EVALUATION METHOD, AND METHOD OF SELECTING INVENTION: PALATABLE RICE THROUGH ANALYSIS OF HALF GRAIN OF UNHULLED/UNPOLISHED RICE
FILE REFERENCE: 227527050X
CURRENT APPLICATION NUMBER: US/10/237,016A
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: JP 2001-273689
PRIOR FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 39
LENGTH: 18

RESULT 14
US-10-237-016-39/c
Sequence 39 Application US/10237016
GENERAL INFORMATION:
APPLICANT: OHSUBO, KENICHI
APPLICANT: OKADOME, HIROSHI
APPLICANT: NAKAMURA, SUMIKO
APPLICANT: HARAGUCHI, KAZUTOMO
APPLICANT: YOZA, KOUTICHI
APPLICANT: OKUNISHI, TOMOYA
APPLICANT: SUZUKI, KEITARO
TITLE OF INVENTION: DNA-LEVEL RICE PALATABILITY EVALUATION METHOD, AND METHOD OF SELECTING INVENTION: PALATABLE RICE THROUGH ANALYSIS OF HALF GRAIN OF UNHULLED/UNPOLISHED RICE
FILE REFERENCE: 227527050X
CURRENT APPLICATION NUMBER: US/10/237,016
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: JP 2001-273689
PRIOR FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 39
LENGTH: 18
TYPE: DNA
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE: OTHER INFORMATION: SYNTHETIC DNA
US-10-237-016A-39

RESULT 13
US-10-217-106-47/c
Sequence 47, Application US/10217106
GENERAL INFORMATION:
APPLICANT: OHSUBO, KENICHI
APPLICANT: NAKAMURA, SUMIKO
APPLICANT: MIYAMURA, TSUYOSHI
APPLICANT: KUMO, SATOSHI
APPLICANT: KATO, IKUNISHI
TITLE OF INVENTION: Method of detecting the presence or absence of mixed varieties in FILE REFERENCE: 226360USX
CURRENT APPLICATION NUMBER: US/10/217,106
CURRENT FILING DATE: 2002-08-13

RESULT 15
US-10-287-187-16018
Sequence 16018 Application US/10287787
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Caulobacter crescentus complete genome
FILE REFERENCE: Jim Zeeber Law Offices - 703-664-8333
CURRENT APPLICATION NUMBER: US/10/287,787
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 27958
SOFTWARE: Proprietary
SEQ ID NO 16018
LENGTH: 19
TYPE: DNA
ORGANISM: Caulobacter crescentus complete genome.

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;FEATURE:  
;LOCATION: (2427911)..  
;OTHER INFORMATION: Chromosome = 1 strand = positive ConnectronObjectNumber = 17744  
US-10-287-787-16018  
Query Match 60 0%; Score 10 8; DB 8; Length 19;  
Best Local Similarity 78.6%; Pred. No. 3e+4;  
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 5 GCCCUAUCCGGUGCGA 18  
||| ||| |||  
Db 4 GCCCATCCGCCGCGA 17
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Job time : 448.636 secs

GenCore version 5.1.4_p5-4578
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On nucleic - nucleic search, using sw model

Run on:

May 22, 2003, 18:59:38 ; Search time 1728.64 Seconds

(without alignments) 218.170 Million cell updates/sec

Title: US-09-780-929-97

Perfect score: 15

Sequence: 1 agauaacgugaagau 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 1600790

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Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	15	100.0	15	US-09-780-929-97	Sequence 97, Appl Sequence 1704, Ap
2	12	80.0	17	US-09-727-026B-1704	Sequence 3093, Ap
3	11.4	76.0	20	US-09-202-228A-3093	Sequence 50, Appl Sequence 13493, A
4	11.4	76.0	20	US-10-003-919-50	Sequence 606, Ap
5	11	73.3	19	US-60-216-745-1493	Sequence 607, Ap
6	10.8	72.0	17	US-09-730-289B-606	Sequence 607, Ap
7	10.8	72.0	17	US-09-730-289B-607	Sequence 607, Ap
8	10.8	72.0	18	US-09-579-536-4	Sequence 4, Appl Sequence 4, Appl Sequence 12, Appl Sequence 4, Appl Sequence 5964, Ap
9	10.8	72.0	18	US-09-579-536C-4	Sequence 50, Appl Sequence 50, Appl Sequence 12, Appl Sequence 4, Appl Sequence 5964, Ap
10	10.8	72.0	18	US-09-668-078-12	Sequence 22, Appl Sequence 50, Appl Sequence 50, Appl Sequence 12, Appl Sequence 4, Appl Sequence 5964, Ap
11	10.8	72.0	18	US-10-213-329-4	Sequence 22, Appl Sequence 50, Appl Sequence 50, Appl Sequence 12, Appl Sequence 4, Appl Sequence 5964, Ap
12	10.8	72.0	18	US-16-745-996	Sequence 22, Appl Sequence 50, Appl Sequence 50, Appl Sequence 12, Appl Sequence 4, Appl Sequence 5964, Ap
13	10.8	72.0	20	US-PCT-US02-03159-22	Sequence 22, Appl Sequence 50, Appl Sequence 50, Appl Sequence 12, Appl Sequence 4, Appl Sequence 5964, Ap
14	10.8	72.0	20	US-09-668-506-50	Sequence 22, Appl Sequence 50, Appl Sequence 50, Appl Sequence 12, Appl Sequence 4, Appl Sequence 5964, Ap
15	10.8	72.0	20	US-09-514-000-12603	Sequence 22, Appl Sequence 50, Appl Sequence 50, Appl Sequence 12, Appl Sequence 4, Appl Sequence 5964, Ap
16	10.8	72.0	20	US-09-514-000-15028	Sequence 22, Appl Sequence 50, Appl Sequence 50, Appl Sequence 12, Appl Sequence 4, Appl Sequence 5964, Ap
17	10.8	72.0	20	US-09-703-708-12172	Sequence 22, Appl Sequence 50, Appl Sequence 50, Appl Sequence 12, Appl Sequence 4, Appl Sequence 5964, Ap
18	10.8	72.0	20	US-60-16-320-12172	Sequence 22, Appl Sequence 50, Appl Sequence 50, Appl Sequence 12, Appl Sequence 4, Appl Sequence 5964, Ap
19	10.8	72.0	20	US-60-183-791-12172	Sequence 22, Appl Sequence 50, Appl Sequence 50, Appl Sequence 12, Appl Sequence 4, Appl Sequence 5964, Ap
20	10.4	69.3	12	PCT-US09-20935-217	Sequence 217, App Sequence 217, App
21	10.4	69.3	12	US-09-215-436-217	Sequence 217, App Sequence 217, App

Query Match 72.0%; Score 10.8; DB 22; Length 18; Best Local Similarity 71.4%; Pred. No. 1e+05; Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0; OQ 2 GAUAACGUGAGAU 15 Db 1 GAGACCGTGAAGAT 14

RESULT 9 US-09-579-536C-4

; Sequence 4, Application US/09579536C

; GENERAL INFORMATION:

; APPLICANT: MACIAG, Thomas

; APPLICANT: ZIMIN, Ann

; APPLICANT: SMALL, Deena

; APPLICANT: PRUDOVSKY, Igor

; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND COMPOSITIONS BASED ON JAGG FILE REFERENCE: 05369-5002-01

CURRENT APPLICATION NUMBER: US/09/579, 536C CURRENT FILING DATE: 2000-05-24

PRIOR APPLICATION NUMBER: US 09/199, 865 PRIOR FILING DATE: 1998-11-25

PRIOR APPLICATION NUMBER: PCT/US97/09407 PRIOR FILING DATE: 1997-03-30

PRIOR APPLICATION NUMBER: US 60/018, 841 PRIOR FILING DATE: 1996-05-31

NUMBER OF SEQ ID NOS: 56 SOFTWARE: Patentin version 3.1 SEQ ID NO 4 LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

; OTHER INFORMATION: PCR primer

US-09-579-536C-4

RESULT 10 Query Match 72.0%; Score 10.8; DB 22; Length 18; Best Local Similarity 71.4%; Pred. No. 1e+05; Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0; OQ 2 GAUAACGUGAGAU 15 Db 1 GAGACCGTGAAGAT 14

US-09-688-076-12

; Sequence 12, Application US/09688078

; GENERAL INFORMATION:

; APPLICANT: Kask, Kalev

; APPLICANT: Melcher, Thorsten

; APPLICANT: Chin, Daniel J.

; TITLE OF INVENTION: DIAGNOSTIC MARKER FOR NEUROLOGICAL CONDITIONS FILE REFERENCE: 019488-00131005 CURRENT APPLICATION NUMBER: US/09/688, 078 CURRENT FILING DATE: 2000-10-13

PRIOR APPLICATION NUMBER: US 60/159, 622 PRIOR FILING DATE: 1999-10-14

NUMBER OF SEQ ID NOS: 22 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 12 LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: PCR primer

; OTHER INFORMATION: upsteam amplification primer 99-25537 for SEQ 1433, US-09-688-078-12

Query Match 72.0%; Score 10.8; DB 22; Length 18; Best Local Similarity 71.4%; Pred. No. 1e+05; Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0; OQ 1 AGUAACGUGAGA 14 Db 1 AGATACGAGAGGA 14

RESULT 11 US-10-213-329-4

; Sequence 4, Application US/10213329

; GENERAL INFORMATION:

; APPLICANT: Maciag, Thomas

; APPLICANT: Zimicin, Ann B.

; APPLICANT: Wong, Michael K.

; APPLICANT: Peiper, Michael S.

; APPLICANT: Montesano, Roberto

; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND COMPOSITIONS BASED ON JAGG FILE REFERENCE: 036-1UL CURRENT APPLICATION NUMBER: US/10/213, 329 CURRENT FILING DATE: 2002-08-06

PRIOR APPLICATION NUMBER: US/09/199, 865 PRIOR FILING DATE: 1998-11-25

PRIOR APPLICATION NUMBER: 60/018, 841 PRIOR FILING DATE: 1996-05-31

PRIOR APPLICATION NUMBER: PCT/US97/09407 PRIOR FILING DATE: 1997-05-30

NUMBER OF SEQ ID NOS: 15 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 4 LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

; OTHER INFORMATION: Description of Artificial sequence: cDNA OTHER INFORMATION: amplification 5'-primer

US-10-213-329-4

RESULT 12 US-60-216-745-5964

; Sequence 5964, Application US/60216745

; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel

; APPLICANT: Blumentfeld, Marta

; APPLICANT: Chumakov, Ilya

; APPLICANT: Abderrahim, Rabi

; APPLICANT: Dufaure-Gare, Isabelle

; TITLE OF INVENTION: BIOMOLECULAR MARKER MAPS FOR USE IN CONSTRUCTING A HIGH DENSITY FILE REFERENCE: 84-US1-PRO CURRENT APPLICATION NUMBER: US/60/216, 745 CURRENT FILING DATE: 2000-06-30

SOFTWARE: Patentin.pm

SEQ ID NO 5964 LENGTH: 18

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

; NAME/KEY: primer_bind LOCATION: 1..18

; OTHER INFORMATION: upstream amplification primer 99-25537 for SEQ 1433, US-60-216-745-5964

APPLICANT: Susan M. Freier
 TITLE OF INVENTION: ANTISENSE MODULATION OF SHIP-1 EXPRESSION
 FILE REFERENCE: RTS_0256
 CURRENT APPLICATION NUMBER: US/10/003,919
 CURRENT FILING DATE: 2001-12-06
 NUMBER OF SEQ ID NOS: 87
 SEQ ID NO 50
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Antisense Oligonucleotide
US-10-003-919-50

Query Match 76.0%; Score 11.4; DB 38; Length 20;
 Best Local Similarity 84.6%; Pred. No. 4.7e+04; 1; Mismatches 1;
 Matches 11; Conservative 1; Indels 0; Gaps 0;
 Qy 2 AGAACGUGAGA 14
 Db 20 GACACAGTGAGA 8

RESULT 5
US-60-216-745-13493
 Sequence 13493, Application US/60216745
 GENERAL INFORMATION:
 APPLICANT: Cohen, Daniel
 APPLICANT: Blumenfeld, Marta
 APPLICANT: Chumakov, Ilya
 APPLICANT: Abderrahim, Hadi
 APPLICANT: Dufaure-Gare, Isabelle
 TITLE OF INVENTION: BIALUBILIC MARKER MAPS FOR USE IN CONSTRUCTING A HIGH DENSITY...
 FILE REFERENCE: 84 US1 PRO
 CURRENT APPLICATION NUMBER: US/60/216,745
 CURRENT FILING DATE: 2000-06-30
 NUMBER OF SEQ ID NOS: 13665
 SOFTWARE: Patent.pw
 SEQ ID NO 13493
 LENGTH: 19
 TYPE: DNA
 ORGANISM: Homo Sapiens
 FEATURE:
 NAME/KEY: primer_bind
 LOCATION: 1..19

OTHER INFORMATION: downstream amplification primer 99-50547 for SEQ 4431, in completer
US-60-216-745-13493

Query Match 73.3%; Score 11; DB 65; Length 19;
 Best Local Similarity 81.8%; Pred. No. 7.8e+04; 0; Mismatches 0;
 Matches 9; Conservative 2; Indels 0; Gaps 0;
 Qy 4 UUACCGUGA 14
 Db 3 TAACCTGAAGA 13

RESULT 6
US-09-730-289B-606/C
 Sequence 606, Application US/09730289B
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Blatt, Larry
 APPLICANT: McSwiggen, Jim
 TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
 FILE REFERENCE: MBHB00-864-A (400/006)
 CURRENT APPLICATION NUMBER: US/09/730,289B
 CURRENT FILING DATE: 2000-12-05
 PRIORITY FILING DATE: 1999-12-06
 NUMBER OF SEQ ID NOS: 3897
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 606

Query Match 72.0%; Score 10.8; DB 29; Length 17;
 Best Local Similarity 71.4%; Pred. No. 1e+05; 2; Mismatches 2;
 Matches 10; Conservative 2; Indels 0; Gaps 0;
 Qy 1 AGAAUACGUGAGA 14
 Db 17 AGATAACATGAGA 4

RESULT 7
US-09-730-289B-607/C
 Sequence 607, Application US/09730289B
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Blatt, Larry
 APPLICANT: McCavigen, Jim
 TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
 FILE REFERENCE: MBHB00-864-A (400/006)
 CURRENT APPLICATION NUMBER: US/09/730,289B
 CURRENT FILING DATE: 2000-12-05
 PRIORITY FILING DATE: 1999-12-06
 NUMBER OF SEQ ID NOS: 3897
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 607

Query Match 72.0%; Score 10.8; DB 29; Length 17;
 Best Local Similarity 71.4%; Pred. No. 1e+05; 2; Mismatches 2;
 Matches 10; Conservative 2; Indels 0; Gaps 0;
 Qy 1 AGAAUACGUGAGA 14
 Db 15 AGATATGTGGAGA 2

RESULT 8
US-09-579-536-4
 Sequence 4, Application US/09579536
 GENERAL INFORMATION:
 APPLICANT: MACTAG, Thomas
 APPLICANT: ZIMRIN, Ann B.
 APPLICANT: SMALL, Deena J.
 APPLICANT: PRUDOVSKY, Igor A.
 TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND COMPOSITIONS
 TITLE OF INVENTION: BASED ON JAGGED/NOTCH PROTEINS AND NUCLEIC ACIDS
 CURRENT APPLICATION NUMBER: US/09/579,536
 CURRENT FILING DATE: 2000-05-24
 PRIORITY FILING DATE: 1998-11-25
 PRIORITY APPLICATION NUMBER: PCT/US97/09407
 PRIORITY FILING DATE: 1997-05-30
 PRIORITY APPLICATION NUMBER: US 60/018,841
 PRIORITY FILING DATE: 1996-05-31
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 4
 LENGTH: 18
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: PCR primer
 US-09-579-536-4